GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:48:12 ; Search time 72 Seconds
(without alignments)
2281.917 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 2424
Sequence: 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2424	100.0	462	7	ADM29326	Adm29326 Human nov
2	2411	99.5	458	2	AAW49908	Aaw49908 Human bra
3	1770.5	73.0	453	2	AAW37254	Aaw37254 Novel non
4	1764.5	72.8	353	7	ADC99051	Adc99051 Human KPP
5	1754.5	72.4	453	2	AAW49906	Aaw49906 Rat prote
6	1598.5	65.9	327	8	ADK71870	Adk71870 Human kin
7	830	34.2	155	2	AAW37255	Aaw37255 Partial h
8	755.5	31.2	802	2	AAY28654	Aay28654 Murine Cy
9	755.5	31.2	802	7	ADL16246	Adl16246 Mouse pro
10	727.5	30.0	807	2	AAW89247	Aaw89247 Human PTP
11	726.5	30.0	799	4	AAG78623	Aag78623 Human tyr
12	710	29.3	773	5	ABB57374	Abb57374 Mouse isc
13	709	29.2	780	3	AAY67252	Aay67252 Human pro
14	709	29.2	780	7	ADC64343	Adc64343 FLJ20037.
15	709	29.2	780	7	ADL16222	Adl16222 Human pro
16	709	29.2	780	7	ADL16220	Adl16220 Human pro
17	709	29.2	780	8	ADH77483	Adh77483 Human PTP
18	708	29.2	692	2	AAY28653	Aay28653 Human Cyt
19	708	29.2	780	4	AAM51205	Aam51205 Human PTP
20	708	29.2	808	2	AAY28652	Aay28652 Human Cyt
21	705.5	29.1	382	7	ADL16228	Adl16228 Rat prote
22	705	29.1	775	3	AAY67250	Aay67250 Mouse pro
23	703	29.0	775	7	ADL16226	Adl16226 Mouse pro
24	700	28.9	780	4	AAM51201	Aam51201 Human PTP
25	699	28.8	780	3	AAY67253	Aay67253 Human mut
26	698	28.8	780	4	AAM51202	Aam51202 Human PTP
27	695	28.7	775	3	AAY67251	Aay67251 Mutant mo
28	665	27.4	312	4	AAG78281	Aag78281 Human PTP
29	658	27.1	253	4	AAB59383	Aab59383 Human pro
30	529	21.8	237	7	ADC64297	Adc64297 Human SID
31	523	21.6	235	5	ADI17283	Adi17283 Polypepti
32	493.5	20.4	313	4	AAG78277	Aag78277 Human SAP
33	491.5	20.3	1093	6	ABR43689	Abr43689 Human tyr
34	491.5	20.3	1118	6	ABR43688	Abr43688 Human tyr
35	489.5	20.2	1115	8	ADN12200	Adn12200 Human Sap
36	486.5	20.1	255	4	AAB59379	Aab59379 Human pro
37	485	20.0	1705	5	ABR52348	Abr52348 Protein r
38	482.5	19.9	613	7	ADL16248	Adl16248 Rat prote
39	474.5	19.6	624	8	ADH50798	Adh50798 Human SHP
40	474	19.6	1711	2	AAW70506	Aaw70506 Osteotest
41	474	19.6	1711	5	ABR52349	Abr52349 Protein r
42	468	19.3	274	4	AAB59385	Aab59385 Protein t
43	467	19.3	595	2	AAR99312	Aar99312 Human SH-
44	464	19.1	1711	2	AAW70507	Aaw70507 Mutant os
45	463.5	19.1	341	4	AAG78283	Aag78283 PTP1. 12/

ALIGNMENTS

RESULT 1
ADM29326
ID ADM29326 standard; protein; 462 AA.
XX
AC ADM29326;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human novel protein NOV11a.
XX
KW human; novel protein; NOV; cancer; immune associated disorder.
XX
OS Homo sapiens.
XX
PN WO2003064628-A2.
XX
PD 07-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-US003401.
XX
PR 01-FEB-2002; 2002US-0353287P.
PR 01-FEB-2002; 2002US-0353301P.
PR 12-FEB-2002; 2002US-0356371P.
PR 12-FEB-2002; 2002US-0356424P.
PR 13-FEB-2002; 2002US-0356531P.
PR 20-FEB-2002; 2002US-0358239P.
PR 26-FEB-2002; 2002US-0359603P.
PR 27-FEB-2002; 2002US-0359848P.
PR 27-FEB-2002; 2002US-0359860P.
PR 15-MAR-2002; 2002US-0365049P.
PR 22-MAR-2002; 2002US-0366802P.
PR 17-MAY-2002; 2002US-0381666P.
PR 18-JUN-2002; 2002US-0389531P.
PR 19-JUN-2002; 2002US-0389910P.
PR 25-JUN-2002; 2002US-0391516P.
PR 02-JUL-2002; 2002US-0393265P.
PR 07-AUG-2002; 2002US-0401825P.
PR 09-AUG-2002; 2002US-0402395P.
PR 12-AUG-2002; 2002US-0402867P.
PR 23-AUG-2002; 2002US-0405401P.
PR 23-AUG-2002; 2002US-0405820P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Bader JS, Berghs C, Burgess CE, Casman SJ;
PI Catterton E, Chaudhuri A, Edinger SR, Ellerman K, Gerlach VL;
PI Gorman L, Guo X, Herrmann JL, Ji W, Khramtsov NV, Li L, Miller CE;
PI Ort T, Patturajan M, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;

PI Spytek KA, Vernet CAM, Zhong H, Zhong M;
XX
DR WPI; 2003-646149/61.
DR N-PSDB; ADM29325.
XX
PT New NOVX polypeptide, useful for the manufacture of a medicament for
PT treating e.g., cancer or immune associated disorders.
XX
PS Claim 1; SEQ ID NO 70; 606pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC human proteins (NOV proteins). The DNA and protein sequences of the
CC invention are useful for the manufacture of a medicament for treating a
CC syndrome associated with a human disease comprising a pathology
CC associated with the protein, such as: cancer or immune associated
CC disorders. The present amino acid sequence represents a NOV protein of
CC the invention.
XX
SQ Sequence 462 AA;

Query Match 100.0%; Score 2424; DB 7; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.1e-222;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420

Qy        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |||||||||||||||||||||||||||||||||||||
Db        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
```

RESULT 2
AAW49908
ID AAW49908 standard; protein; 458 AA.
XX
AC AAW49908;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human brain derived phosphatase 1 (BDP-1).
XX
KW Brain derived phosphatase 1; BDP-1; human; receptor;
KW protein tyrosine phosphatase; signal transduction; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9748723-A2.

XX
PD 24-DEC-1997.
XX
PF 17-JUN-1997; 97WO-IB000946.
XX
PR 17-JUN-1996; 96US-0019629P.
PR 09-AUG-1996; 96US-0023485P.
PR 13-NOV-1996; 96US-0030860P.
PR 15-NOV-1996; 96US-0030964P.
PR 19-DEC-1996; 96US-0034286P.
XX
PA (PLAC') MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Ullrich A, Kharitonenkov AI, Aoki N, Wang HY, Chen Z, Nayler O;
PI Kim YW;
XX
DR WPI; 1998-120302/11.
DR N-PSDB; AAV17099.
XX
PT New phosphatase and kinase enzyme(s) - useful in the diagnosis and
PT treatment of signal transduction disorders.
XX
PS Claim 11; Fig 3a-d; 138pp; English.
XX
CC This polypeptide comprises a novel human protein tyrosine phosphatase
CC (PTP), designated brain derived phosphatase 1 (BDP-1), that is expressed
CC in most tissues and cell lines at basal level, but expressed high in
CC epithelium origin cell lines and cancer cell lines. The amino acid
CC sequence was deduced from a cDNA clone (see AAV17099) isolated from a
CC haematopoietic MEG01 cDNA library. The invention relates to novel
CC proteins (see AAW49906-14) involved in cellular signal transduction and
CC to the nucleic acids (see AAV17097-99) coding for them, and provides
CC vectors, host cells, purified recombinant proteins, methods for
CC identifying compounds that activate or inhibit the novel proteins, as
CC well as methods for the diagnosis and treatment of diseases associated
CC with the novel proteins
XX
SQ Sequence 458 AA;

Query Match 99.5%; Score 2411; DB 2; Length 458;
Best Local Similarity 99.8%; Pred. No. 1.2e-220;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAHKADGVCSTVAGSRPENVRKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420

Qy        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |||||||||||||||||||||||||||||||||||||
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```
Db        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458

RESULT 3
AAW37254
ID   AAW37254 standard; protein; 453 AA.
XX
AC   AAW37254;
XX
DT   09-APR-1998  (first entry)
XX
DE   Novel non-receptor tyrosine phosphatase of hematopoietic stem cells.
XX
KW   Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
KW   PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;
KW   tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
KW   stem cell differentiation.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Domain          6. .303
FT                   /note= "tyrosine phosphatase domain"
FT   Active-site     37
FT                   /note= "phosphorylated by protein kinases A and C; also
FT                   appears to negatively regulate PTPase activity"
FT   Active-site     229
FT                   /note= "active site cysteine residue"
FT   Region          312. .428
FT                   /note= "Pro, Ser and Thr rich region"
FT   Region          430. .450
FT                   /note= "homologous to a nuclear localization signal found
FT                   on murine PTP PEP"
XX
PN   WO9735019-A1.
XX
PD   25-SEP-1997.
XX
PF   17-MAR-1997;   97WO-US005278.
XX
PR   22-MAR-1996;   96US-00620526.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Lasky LA,  Cheng J;
XX
DR   WPI; 1997-480224/44.
DR   N-PSDB; AAV03112.
XX
PT   Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
PT   useful for expansion of undifferentiated stem cells in cell culture.
XX
PS   Claim 9; Fig 1; 66pp; English.
XX
CC   The present sequence represents a novel murine non-receptor protein
CC   tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
CC   is predominantly expressed in early hematopoietic stem cells (HSCs) or
CC   progenitor cells, and lacks expression in adult tissues. The protein has
CC   a N-terminal tyrosine phosphatase domain, followed by a region rich in
CC   serine, threonine and proline and a C-terminal region of about 15-25
CC   amino acids which is rich in basic amino acid residues. The protein is
CC   capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
CC   and functional derivatives of such native tyrosine phosphatases. The
CC   phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
CC   progenitor cell can be used in an assay for the identification of PTP HSC
CC   antagonists or agonists. The antagonist can be used to induce the
CC   differentiation of stem cells, such as undifferentiated malignant
CC   hematopoietic cells, e.g. leukaemia cells, which may facilitate their
CC   treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
CC   used for the expansion of undifferentiated stem cells in cell culture
CC   (this allows expansion of HSC prior to autologous or heterologous bone
CC   marrow transplantation), while the agonist antibody along with a
CC   hematopoietic growth factor can be used for the expansion of
CC   undifferentiated stem cells in vivo
XX
SQ   Sequence 453 AA;

  Query Match             73.0%;  Score 1770.5;  DB 2;  Length 453;
  Best Local Similarity   74.7%;  Pred. No. 1.4e-159;
  Matches  343;  Conservative   32;  Mismatches   77;  Indels    7;  Gaps    2;

Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
              |||  |  |||||:||||  ||||:  |||||:| | |||::||||| ||||  |  ||
Db          1 MSRHTDLVRSFLEQLEARDYREGAIFVREFSDIKARSVAWKSEGVCSTKAGSRLGNTNKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
              |||||: ||:|||||||||||||| :||| |||||:||| ||||||||||||||||||||
Db         61 RYKDVVAYDETRVILSLLQEEGHGNYINANFIRGIDGSQAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
              |||||||||||:| ||||::||||||:|||||: | ||||| ||  || || ||||:|||
Db        121 EFGVKVILMACQETENGRRKCERYWAREQEPLKAGPFCITLTKETTLNADITLRTLQVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
              ||| |||:||||||||| ||||| ||:| |||||| ||| || ||||||||||||||||
Db        181 QKEFRSVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              |||||||||| |||:|||| |||:|||||||||||||||||||||:| |||: |
Db        241 AVDYVRQLLLTQTIPPNFSLFQVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQDTS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
              | |||:||||||:  :|  |||  || |  |||||||||||  |  ||||||  |||
Db        301 PQYQNLKENCAPICKEAFSLRTSSALPATSRPPGGVLRSISVPAPPTLPMADTYAVVQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
              || || | |  :  | |      : |:||:| |||||| || |||:||     ||||||: :
Db        361 GASAGTGPGPRAPTST------DTPIYSQVAPRAQRPVAHTEDAQGTTALRRVPADQNSS 414

Qy        420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |  |||:|  ||||||||||||||||||||||||||||
Db        415 GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453


RESULT 4
ADC99051
ID   ADC99051 standard; protein; 353 AA.
XX
AC   ADC99051;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Human KPP protein - SEQ ID 4.
XX
KW   anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;
KW   nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW   immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW   antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
KW   osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;
KW   uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
KW   virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
KW   cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
KW   cancer; developmental; mental retardation; neurological;
KW   Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
KW   diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
KW   helminthic infection; transgenic; gene therapy; human; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2003033680-A2.
XX
PD   24-APR-2003.
XX
PF   17-OCT-2002; 2002WO-US033723.
XX
PR   19-OCT-2001; 2001US-0345474P.
```

PR 02-NOV-2001; 2001US-0343910P.
PR 13-NOV-2001; 2001US-0333098P.
PR 16-NOV-2001; 2001US-0332424P.
PR 30-NOV-2001; 2001US-0334288P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
PI Zebarjadian Y;
XX
DR WPI; 2003-403214/38.
DR N-PSDB; ADC99103.
XX
PT New human kinases and phosphatases and polynucleotides, useful for
PT diagnosing, treating or preventing autoimmune or inflammatory disorders
PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
PT cancer or hepatitis.
XX
PS Claim 1; SEQ ID NO 4; 424pp; English.
XX
CC The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
CC agonists and antagonists are useful for diagnosing, treating or
CC preventing cell proliferative disorders such as atherosclerosis,
CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
CC retardation, neurological disorders including Alzheimer's disease and
CC Parkinson's disease, autoimmune and inflammatory disorders such as
CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
CC polynucleotides encoding KPP may be useful for creating transgenic
CC animals to model human disease, as well as during gene therapy
CC procedures. The current sequence is that of the human KPP protein of the
CC invention.
XX
SQ Sequence 353 AA;

Query Match 72.8%; Score 1764.5; DB 7; Length 353;
Best Local Similarity 75.9%; Pred. No. 3.7e-159;
Matches 349; Conservative 0; Mismatches 2; Indels 109; Gaps 2;

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Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
              ||||||||||||||||||||||||||||||
Db          1 MSRSLDSARSFLERLEARGGREGAVLAGEFS---------------------------- 31

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120

Db         32 ------------------------------------------------------------ 31

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
                                 ||||||||||||||||||||||||||||||||||||||||
Db         32 ------------------KRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 73

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 133

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 193

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        194 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAVVQKR 253

Qy        361 GAPAGAGSGTQ--TGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSP 418
              ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 GAPAGAGSGTQTGTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSP 313

Qy        419 AGSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |||||||||||||||||||||||||||||||||||||||||
Db        314 AGSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 353
```

RESULT 5
AAW49906
ID AAW49906 standard; protein; 453 AA.
XX
AC AAW49906;
XX
DT 20-JUL-1998 (first entry)
XX
DE Rat protein tyrosine phosphatase PRP20.
XX
KW Protein tyrosine phosphatase; PTP20; rat; signal transduction;
KW cell differentiation; cancer; neural injury; therapy.
XX
OS Rattus sp.
XX
PN WO9748723-A2.
XX
PD 24-DEC-1997.
XX
PF 17-JUN-1997; 97WO-IB000946.
XX
PR 17-JUN-1996; 96US-0019629P.
PR 09-AUG-1996; 96US-0023485P.
PR 13-NOV-1996; 96US-0030860P.
PR 15-NOV-1996; 96US-0030964P.
PR 19-DEC-1996; 96US-0034286P.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Ullrich A, Kharitonenkov AI, Aoki N, Wang HY, Chen Z, Nayler O;
PI Kim YW;
XX
DR WPI; 1998-120302/11.
DR N-PSDB; AAV17097.
XX
PT New phosphatase and kinase enzyme(s) - useful in the diagnosis and
PT treatment of signal transduction disorders.
XX
PS Claim 11; Fig 1a-b; 138pp; English.
XX
CC This polypeptide comprises a novel rat protein tyrosine phosphatase,
CC designated PTP20, that regulates growth factor stimulation of cellular
CC differentiation. Its amino acid sequence was deduced from a cDNA clone
CC (see AAV17097) isolated from a rat phaeochromocytoma PC12 cDNA library by
CC PCR amplification using primers based on consensus sequences (see
CC AAW49915-16) of known PTPs. The invention relates to novel proteins (see
CC AAW49906-14) involved in cellular signal transduction and to the nucleic
CC acids (see AAV17097-99) coding for them, and provides vectors, host
CC cells, purified recombinant proteins, methods for identifying compounds
CC activate or inhibit the novel proteins, as well as methods for the
CC diagnosis and treatment of diseases associated with the novel proteins.
CC For PTP20, activators may act as anti-cancer therapeutics that stimulate
CC cell differentiation rather than proliferation, while inhibitors may be
CC useful for treating neural injuries by delaying the differentiation of
CC transplanted neuronal stem cells until they are firmly grafted
XX
SQ Sequence 453 AA;

Query Match 72.4%; Score 1754.5; DB 2; Length 453;
Best Local Similarity 74.5%; Pred. No. 4.8e-158;
Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;

```
Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
              |||  |  |||||: |||  |:||:|| |||||:| | ||| :||||| |||:  | :||
Db          1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAWKTEGVCSTKAGSQQGNSKKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
              |||||:|||:|||||||||||||| |||| ||||| ||| ||||||||||||||||||||
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```
Db         61 RYKDVVPYDETRVILSLLQEEGHGDYINANFIRGTDGSQAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180

Db        121 EFGIKVILMACQETENGRRKCERYWAQEREPLQAGPFCITLTKETALTSDITLRTLQVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240

Db        181 QKESRPVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300

Db        241 AVDYVRQLLLTQTIPPNFSLFEVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQNNS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360

Db        301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLRSISVPGPPTLPMADTYAVVQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419

Db        361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTENAQGTTALGRVPADENPS 414

Qy        420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458

Db        415 GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453
```

RESULT 6
ADK71870
ID ADK71870 standard; protein; 327 AA.
XX
AC ADK71870;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human kinase and phosphatase KPP-47 protein.
XX
KW human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
KW hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV;
KW antiallergic; antiasthmatic; immunosuppressive; antithyroid;
KW dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal;
KW neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological;
KW antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
KW antipsoriatic; haemostatic; cytostatic; antilipaemic; antiparasitic;
KW antihelmintic; antibacterial; virucide; protozoacide; fungicide;
KW cardiovascular disease; immune system; neurological; growth; development;
KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; enzyme.
XX
OS Homo sapiens.
XX
PN WO2004018641-A2.
XX
PD 04-MAR-2004.
XX
PF 25-AUG-2003; 2003WO-US026635.
XX
PR 26-AUG-2002; 2002US-0406172P.
PR 25-SEP-2002; 2002US-0413910P.
PR 27-SEP-2002; 2002US-0414296P.
PR 11-OCT-2002; 2002US-0417821P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
PI Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
PI Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
PI Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
PI Murage J;
XX
DR WPI; 2004-226830/21.
DR N-PSDB; ADK71929.
XX
PT New human kinases and phosphatases, useful for diagnosing, treating or
PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple
PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
PT or hepatitis.
XX
PS Claim 1; SEQ ID NO 47; 347pp; English.
XX
CC The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (KPP). The polypeptide of the invention
CC demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
CC vasotropic, antiinflammatory, antianginal, anti-HIV, antiallergic,
CC antiasthmatic, immunosuppressive, antithyroid, dermatological,
CC antidiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective,
CC osteopathic, antiarthritic, uropathic, ophthalmological, antirheumatic,
CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic,
CC haemostatic, cytostatic, antilipaemic, antiparasitic, antihelmintic,
CC antibacterial, virucide, protozoacide and fungicide activities. The
CC kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
CC antagonists may be useful for diagnosing, treating or preventing
CC disorders such as cardiovascular diseases, immune system disorders,
CC neurological disorders, disorders affecting growth and development, cell
CC proliferative disorders and viral, bacterial, fungal, parasitic,
CC protozoan or helminthic infections. Furthermore, the molecules of the
CC invention may be useful for creating transgenic animals to model human
CC disease and during gene therapy. The current sequence is that of a human
CC KPP protein of the invention.
XX
SQ Sequence 327 AA;

Query Match 65.9%; Score 1598.5; DB 8; Length 327;
Best Local Similarity 69.8%; Pred. No. 2.3e-143;
Matches 321; Conservative 0; Mismatches 4; Indels 135; Gaps 3;

```
Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60

Db          1 MSRSLDSARSFLERLEARGGREGAVLAGEFS---------------------------- 31

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120

Db         32 ------------------------------------------------------------ 31

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180

Db         32 ------------------KRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 73

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240

Db         74 QKGSRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 133

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300

Db        134 TVDYVRQLLLTQ------------------------EQYRFLYHTVAQMFCSTLQNAS 167

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360

Db        168 PHYQNIKENCAPLYDDALFLRAPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAVVQKR 227

Qy        361 GAPAGAGSGTQ--TGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSP 418

Db        228 GAPAGAGSGTQTGTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSP 287

Qy        419 AGSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458

Db        288 AGSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 327
```

RESULT 7
AAW37255
ID AAW37255 standard; protein; 155 AA.
XX
AC AAW37255;
XX
DT 09-APR-1998 (first entry)

```
XX
DE   Partial human non-receptor tyrosine phosphatase.
XX
KW   Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
KW   PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;
KW   tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
KW   stem cell differentiation.
XX
OS   Homo sapiens.
XX
PN   WO9735019-A1.
XX
PD   25-SEP-1997.
XX
PF   17-MAR-1997;   97WO-US005278.
XX
PR   22-MAR-1996;   96US-00620526.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Lasky LA,  Cheng J;
XX
DR   WPI; 1997-480224/44.
DR   N-PSDB; AAV03128.
XX
PT   Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
PT   useful for expansion of undifferentiated stem cells in cell culture.
XX
PS   Claim 9; Fig 8; 66pp; English.
XX
CC   The present sequence represents a partial human non-receptor protein
CC   tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
CC   is predominantly expressed in early hematopoietic stem cells (HSCs) or
CC   progenitor cells, and lacks expression in adult tissues. The protein has
CC   a N-terminal tyrosine phosphatase domain, followed by a region rich in
CC   serine, threonine and proline and a C-terminal region of about 15-25
CC   amino acids which is rich in basic amino acid residues. The protein is
CC   capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
CC   and functional derivatives of such native tyrosine phosphatases. The
CC   phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
CC   progenitor cell can be used in an assay for the identification of PTP HSC
CC   antagonists or agonists. The antagonist can be used to induce the
CC   differentiation of stem cells, such as undifferentiated malignant
CC   hematopoietic cells, e.g. leukaemia cells, which may facilitate their
CC   treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
CC   used for the expansion of undifferentiated stem cells in cell culture
CC   (this allows expansion of HSC prior to autologous or heterologous bone
CC   marrow transplantation), while the agonist antibody along with a
CC   hematopoietic growth factor can be used for the expansion of
CC   undifferentiated stem cells in vivo
XX
SQ   Sequence 155 AA;

  Query Match             34.2%;  Score 830;  DB 2;  Length 155;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-70;
  Matches  155;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 60

Qy         77 LLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIEN 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIEN 120

Qy        137 GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 171
              |||||||||||||||||||||||||||||||||||
Db        121 GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 155


RESULT 8
AAY28654
ID   AAY28654 standard; protein; 802 AA.
XX
AC   AAY28654;
XX
DT   01-OCT-1999  (first entry)
XX
DE   Murine Cytoplasmic phosphatase, Z70PEP protein.
XX
KW   Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell;
KW   intracellular tyrosine phosphatase; PTPase; lymphocyte; murine;
KW   protein tyrosine kinase; PTKs; immunosuppressant; PEST sequence;
KW   T cell antigen receptor signalling; autoimmune disease; transplant;
KW   cytokine receptor signalling.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Domain          27. .288
FT                   /label= PTPase_domain
FT                   /note= "Catalytic protein tyrosine phosphatase domain"
FT   Binding-site    613. .621
FT                   /label= SH3_binding_site
FT                   /note= "Proline rich sequence"
FT   Binding-site    689. .695
FT                   /label= SH3_binding_site
FT                   /note= "Proline rich sequence"
FT   Binding-site    790. .798
FT                   /label= SH3_binding_site
FT                   /note= "Proline rich sequence"
XX
PN   WO9936548-A1.
XX
PD   22-JUL-1999.
XX
PF   18-JAN-1999;   99WO-CA000038.
XX
PR   16-JAN-1998;   98CA-02220853.
XX
PA   (HSCR-) HSC RES & DEV LP.
XX
PI   Roifman CM;
XX
DR   WPI; 1999-444404/37.
XX
PT   New nucleic acid encoding intracellular tyrosine phosphatase and related
PT   proteins, used to modulate signaling through T cells, particularly as
PT   immunosuppressant.
XX
PS   Disclosure; Page 63-64; 105pp; English.
XX
CC   The present protein sequence is that of the murine phosphatase, Z70PEP
CC   that has a single catalytic domain. The non-catalytic portion of the
CC   phosphatase contains unique sequences, including five PEST sequences rich
CC   in Pro, Glu or Asp, Ser and Thr. Z70PEP shares about 70% sequence
CC   identity with the human cytoplasmic phosphatase Lyp1. Lyp proteins are
CC   important for regulation of T cell antigen and cytokine receptor
CC   signalling and for early and late stages of T cell differentiation.
CC   Z70PEP has immunosuppressive activity. Compounds that increase expression
CC   of Lyp protein can be used as immunosuppressive agents to reduce or
CC   prevent T cell activation or proliferation, to control thymocyte
CC   differentiation, to treat autoimmune diseases and transplant situations
XX
SQ   Sequence 802 AA;

  Query Match             31.2%;  Score 755.5;  DB 2;  Length 802;
  Best Local Similarity   44.0%;  Pred. No. 2.1e-62;
  Matches  161;  Conservative   55;  Mismatches  119;  Indels   31;  Gaps    7;

Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :||| :  |    ||:|::||||||:|||| : | ||||  :  | |
Db         25 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || :||:|| |  |||||||||  ||||||||::||: : ||:||| | | |:|:||||||
```

```
Db         85 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  || | | |:   ||    | :|||  |  |:| :||  | :|||  |||| |
Db        145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
              :| :: : |  |     |:|:||||||||||:| |||   ||   :|| :||:|:::
Db        204 PILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 263

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325
              :|| |||: |||:|||  :|  | ::|          |   | :|             |  ||
Db        264 EMRTQRPSLVQTQEQYELVYSAVLELF-------KRHMDVISDNHLG--------REIQA 308

Qy        326 LLAIPRPPGGVLRSISVPGS------PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377
              :||       :|::|         | :|| |  |  :  |:|| | :  |:  |  |
Db        309 QCSIPE------QSLTVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGLRTS 362

Qy        378 ARSAEE 383
              :|||
Db        363 TMNAEE 368
```

RESULT 9
ADL16246
ID ADL16246 standard; protein; 802 AA.
XX
AC ADL16246;
XX
DT 06-MAY-2004 (first entry)
XX
DE Mouse protein tyrosine phosphatase #7.
XX
KW cytostatic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormalit.
XX
OS Mus musculus.
XX
PN WO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
PR 12-FEB-2003; 2003US-00366547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
DR N-PSDB; ADL16245.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 95; 238pp; English.
XX
CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. . No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
SQ Sequence 802 AA;

Query Match 31.2%; Score 755.5; DB 7; Length 802;
Best Local Similarity 44.0%; Pred. No. 2.1e-62;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

```
Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :||| :   |    ||:|::|||||:|||| : | ||||  :  | |
Db         25 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || :||:|| |  |||||||||  |||||||::||: : ||:||| | | |:|:||||||
Db         85 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  || | | |:   ||    | :|||  |  |:| :||  | :|||  |||| |
Db        145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
              :| :: : |  |     |:|:||||||||||:| |||   ||   :|| :||:|:::
Db        204 PILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 263

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325
              :|| |||: |||:|||  :|  | ::|          |   | :|             |  ||
Db        264 EMRTQRPSLVQTQEQYELVYSAVLELF-------KRHMDVISDNHLG--------REIQA 308

Qy        326 LLAIPRPPGGVLRSISVPGS------PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377
              :||       :|::|         | :|| |  |  :  |:|| | :  |:  |  |
Db        309 QCSIPE------QSLTVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGLRTS 362

Qy        378 ARSAEE 383
              :|||
Db        363 TMNAEE 368
```

RESULT 10
AAW89247
ID AAW89247 standard; protein; 807 AA.
XX
AC AAW89247;
XX
DT 10-MAR-1999 (first entry)
XX
DE Human PTP04.
XX
KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease.
XX
OS Homo sapiens.
XX
PN WO9849317-A2.
XX
PD 05-NOV-1998.
XX
PF 27-APR-1998; 98WO-US008439.
XX
PR 28-APR-1997; 97US-0044428P.
PR 20-MAY-1997; 97US-0047222P.
PR 11-JUN-1997; 97US-0049477P.
PR 11-JUN-1997; 97US-0049756P.
PR 18-JUN-1997; 97US-0049914P.

PR 23-OCT-1997; 97US-0063595P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
PI Courtneidge SA, App H, Hui TH;
XX
DR WPI; 1999-009434/01.
DR N-PSDB; AAV81742.
XX
PT New nucleic acid encoding specific protein tyrosine phosphatases - useful
PT for identifying specific modulators for treatment and prevention of
PT cancer and neurodegenerative disease.
XX
PS Claim 2; Page 151-153; 193pp; English.
XX
CC The present invention describes isolated, enriched or purified nucleic
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
CC present sequence represents human PTP04. The above proteins, other than
CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify
CC substances that modulate their activity (i.e. agonists and antagonists,
CC including NBP) in vivo or in vitro. These substances are used to treat or
CC prevent diseases associated with abnormal signal transduction pathways
CC that involve the proteins, particularly cancer (e.g. leukaemia and
CC lymphoma), while modulators of ALK-7 (which is a type I receptor
CC serine/threonine kinase) are used to promote neuronal survival,
CC particularly for treating Alzheimer's, Parkinson's or Huntington's
CC diseases. Nucleic acid fragments of the polynucleotides encoding the
CC proteins can be used as probes to identify and clone related sequences;
CC to detect protein-encoded RNA; to generate transgenic animals and in gene
CC therapy (optionally after mutation). Ab are used to determine the
CC proteins
XX
SQ Sequence 807 AA;

Query Match 30.0%; Score 727.5; DB 2; Length 807;
Best Local Similarity 46.9%; Pred. No. 9.9e-60;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;

Qy 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
Db 25 ANEFLKLKRQSTKYKADKTYPTTVAEKPKNIKKNRYKDILPYDYSRVELSLITSDEDSSY 84

Qy 87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
Db 85 INANFIKGVYGPEAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWA 144

Qy 147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
Db 145 EPGEMQLEFGPFSVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID 203

Qy 206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
Db 204 PILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIDYTWMLLKDGIIPENFSVFSLIR 263

Qy 266 KMRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
Db 264 EMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKHSGTESQAKHCIP 313

RESULT 11
AAG78623
ID AAG78623 standard; protein; 799 AA.
XX
AC AAG78623;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human tyrosine phosphatase.
XX
KW Human; tyrosine phosphatase; hPTP.
XX
OS Homo sapiens.
XX
PN CN1302899-A.
XX
PD 11-JUL-2001.
XX
PF 29-OCT-1999; 99CN-00119935.
XX
PR 29-OCT-1999; 99CN-00119935.
XX
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
XX
PI Ren S, Wu T, Qian B;
XX
DR WPI; 2001-550591/62.
DR N-PSDB; AAH79342.
XX
PT Human protein tyrosine phosphatase and its coding sequence.
XX
PS Claim 4; Page 12-13(Disclosure); 29pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC tyrosine phosphatase hPTP. The protein is expressed in human normal
CC suprarenal tissue. The present sequence is the protein of the invention
XX
SQ Sequence 799 AA;

Query Match 30.0%; Score 726.5; DB 4; Length 799;
Best Local Similarity 46.9%; Pred. No. 1.2e-59;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;

Qy 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
Db 25 ANEFLKLKRQSTKYKADKTYPTTVAEKPKNIKKNRYKDILPYDYSRVELSLITSDEDSSY 84

Qy 87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
Db 85 INANFIKGVYGPEAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWA 144

Qy 147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
Db 145 EPGEMQLEFGPFSVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID 203

Qy 206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
Db 204 PILELIWDVRCTQEDDSVPICIHCSAGCGRTGVICAIDYTWMLLKDGIIPENFSVFSLIR 263

Qy 266 KMRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
Db 264 EMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKHSGTESQAKHCIP 313

RESULT 12
ABB57374
ID ABB57374 standard; protein; 773 AA.
XX
AC ABB57374;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related protein sequence SEQ ID NO:1064.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP004192.
XX
PR 18-MAY-2000; 2000JP-00145977.

```
XX
PA   (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI   Ishikawa K,  Asai S,  Takahashi Y,  Nagata T,  Ishii Y;
XX
DR   WPI; 2002-034733/04.
DR   N-PSDB; ABI99910.
XX
PT   Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT   expression levels of particular genes defined in the specification or by
PT   determining the expression profile of a gene group comprising these
PT   genes.
XX
PS   Claim 2; Page 2685-2689; 2690pp; English.
XX
CC   The present invention describes a method for examining ischaemic
CC   conditions, comprising measuring the expression levels of particular
CC   genes (I) in a test sample or determining the expression profile of a
CC   gene group in the sample comprising genes selected from (I). The method
CC   is useful for examining the ischaemic condition (e.g. compressive
CC   ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC   expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC   protein sequences in ABB57020 to ABB57374) or by determining the
CC   expression profile of a gene group comprising these genes. The expression
CC   levels or expression profiles produced by these genes are used as an
CC   indicator when screening for ischaemic condition-improving drugs or
CC   therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC   primers for a mouse ischaemic condition related sequence, which are used
CC   in the exemplification of the present invention
XX
SQ   Sequence 773 AA;

  Query Match             29.3%;  Score 710;  DB 5;  Length 773;
  Best Local Similarity   25.4%;  Pred. No. 4.3e-58;
  Matches  195;  Conservative   88;  Mismatches  162;  Indels  324;  Gaps   20;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :   | :|  ::  |  :: : :  |  | : |||:|||||
Db          8 RRFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|     |||||  |||:|| |  ||:|||||  :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPFRNTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:||||| | |||:|||||    ::|:    | |:   |:     |  :||| : ||
Db        126 VVMIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:   |: |     |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMF---------- 292
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :||:|
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFENSYNCMKFM 304

Qy        293 ------------------------------------------------------------ 292

Db        305 EHRRSVMVMKLPLELWSVPLIARRDLSAKAAADSKLPCRRGCQGRNTTATRTSPGATHPD 364

Qy        293 -------------CSTLQNAS-------PHYQN--------------------------- 305
                          | |:   :       ||  |
Db        365 AITSFSLPNVTTVCRTVTGTTQSQCCTWPHQSNTQPTSTEAMINQRTNGAKSESAIEHID 424

Qy        306 --IKENCA------PL------YDDALFL-----------------RT--PQALLA---- 328
                :: | :      ||      :|    |                 ||  || | |
Db        425 KKLERNLSFEIKKVPLQEGPKSFDGNTLLNRGHAIKIKSASSSVVDRTSKPQELSAGALK 484

Qy        329 ---------------------------------IPRP-------PGGVLRSI-------S 341
                                              |||       | | |:
Db        485 VDDVSQNSCADCSAAHSHRAAESSEESQSNSHTPPRPDCLPLDKKGHVTWSLHGPENATP 544

Qy        342 VPGSPGHAMADTY-------------AEEQKR-------------------------- 360
                 || ||     | :                |||:
Db        545 VPDSPDGKSPDNHSQTLKTVSSTPNSTAEEEAHDLTEHHNSSPLLKAPLSFTNPLHSDDW 604

Qy        361 ----GAPAGAGSGTQTGTGTGA-----RSAEEAPLYSKVTPR-------------AQRP 397
                  |:  || :  :|   | :       |: |:  : :| ||              |::
Db        605 HSDGGSSDGAVTRNKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTPHSGAEKD 664

Qy        398 GAHAEDARGTLPGRVP---------------------------------------------- 413
                 :|::   || | |
Db        665 ADVSEESPPPLPERTPESFVLADMPVRPEWHELPNQEWSEQRESEGLTTSGNEKHDAGGI 724

Qy        414 -----ADQSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT 456
                   ||  || |   : :    |:   :||  | |:|||||:||:|||
Db        725 HTEASADSPPAFSDKKDQITKSPAEVTDIGFGNRCGKPKGPREPPSEWT 773


RESULT 13
AAY67252
ID   AAY67252 standard; protein; 780 AA.
XX
AC   AAY67252;
XX
DT   05-APR-2000  (first entry)
XX
DE   Human protein tyrosine phosphatase (PTP) PEST amino acid sequence.
XX
KW   Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion;
KW   cell migration; division; cytostatic; antiinflammatory; angiogenesis;
KW   cancer; enzyme substrate identification; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          333. .340
FT                   /label= Pro_1
FT                   /note= "Proline rich domain 1"
FT   Domain          356. .365
FT                   /label= Pro_2
FT                   /note= "Proline rich domain 2"
FT   Domain          519. .528
FT                   /label= Pro_3
FT                   /note= "Proline rich domain 3"
FT   Domain          674. .680
FT                   /label= Pro_4
FT                   /note= "Proline rich domain 4"
FT   Domain          769. .776
FT                   /label= Pro_5
FT                   /note= "Proline rich domain 5"
XX
PN   WO9961467-A2.
XX
PD   02-DEC-1999.
XX
PF   21-MAY-1999;   99WO-CA000461.
XX
PR   21-MAY-1998;   98CA-02238654.
PR   11-DEC-1998;   98US-0111993P.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Tremblay ML,  Cote J,  Angers-Lousteau A,  Charest A;
XX
DR   WPI; 2000-097104/08.
XX
PT   Novel therapeutic agents for treating diseases which are related to cell
PT   proliferation, migration, inflammation and angiogenesis especially
PT   cancer.
XX
PS   Claim 4; Fig 24; 91pp; English.
XX
CC   This is the amino acid sequence of human protein tyrosine phosphatase
CC   (PTP) PEST. PTP-PEST is a soluble PTP that is ubiquitously expressed
CC   throughout embryonic development and in murine adult tissues. The N-
```

```
CC   terminal portion of the enzyme encodes for the catalytic domain, while
CC   the C-terminal portion is composed of 5 proline rich domains, and a
CC   binding site for the adaptor protein Shc. The pro 2 domain is required
CC   for paxillin binding, and the synthesis of mutant PTP-PEST have shown
CC   that proline 362 is important for paxillin binding activity. The
CC   invention relates to a compound that is capable of interfering with the
CC   binding of PTP-PEST to signalling molecules that are involved in cell
CC   migration, adhesion or division. The compound can be derived from minimal
CC   sequences found in binding sites of PTP-PEST. The invention also relates
CC   to a method for finding a genuine substrate for an enzyme in a cell that
CC   normally expresses the wild type form of the enzyme. A mutant version of
CC   PTP-PEST (see AAY67251 and AAY67253) is used in this method. The
CC   compounds have cytostatic and antiinflammatory activity. The compounds
CC   are used for making medicaments for treating a disease related with cell
CC   proliferation, migration, inflammation and angiogenesis, especially
CC   cancer. The novel method is used for identifying a genuine substrate for
CC   an enzyme
XX
SQ   Sequence 780 AA;

  Query Match             29.2%;  Score 709;  DB 3;  Length 780;
  Best Local Similarity   40.7%;  Pred. No. 5.5e-58;
  Matches  143;  Conservative   66;  Mismatches  116;  Indels   26;  Gaps    7;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :    | :|  ::  |  :: : :  |  | : |||:|||||
Db          8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|     ||||| |||:|| |  ||:|||||| :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:|||| | |||:|||||    ::|:    | |:  :::    |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |:|||  |||| | :| |:   |: |     |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :||:|   ||    |
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        303 YQNIKENCAPLYDDALFLRTPQALLAI---------PRPPGGVLRSISVPG 344
                    : |    : |  : :|         |:||    ||  | |
Db        305 ------GAQKIADGVNEINTENMISSIEPEKQDSPPPKPPR--TRSCLVEG 347


RESULT 14
ADC64343
ID   ADC64343 standard; protein; 780 AA.
XX
AC   ADC64343;
XX
DT   18-DEC-2003  (first entry)
XX
DE   FLJ20037.
XX
KW   Hepatotropic; vaccine; protein-protein interaction;
KW   Transforming Growth Factor beta; TGF beta; hepatitis;
KW   Selected Interacting Domain; SID.
XX
OS   Unidentified.
XX
PN   WO2003045990-A2.
XX
PD   05-JUN-2003.
XX
PF   26-NOV-2002; 2002WO-EP013866.
XX
PR   26-NOV-2001; 2001US-0333348P.
PR   31-MAY-2002; 2002US-0384537P.
PR   30-OCT-2002; 2002US-0422471P.
XX
PA   (HYBR-) HYBRIGENICS.
XX
PI   Legrain P,  Gauthier J,  Colland F,  Jacq X;
XX
DR   WPI; 2003-505185/47.
DR   N-PSDB; ADC64342.
XX
PT   New complex between two interacting proteins, useful for screening
PT   molecules that inhibit transforming growth factor beta (TGF beta) or TGF
PT   beta super-family of cytokines pathway for diagnosing or treating TGF
PT   beta diseases or disorders.
XX
PS   Example 16; SEQ ID NO 127; 148pp; English.
XX
CC   The present invention relates to protein-protein interactions and
CC   complexes involved in Transforming Growth Factor (TGF) beta disorders
CC   and/or diseases. The complex between two interacting proteins is useful
CC   for screening molecules that inhibit TGF beta for diagnosing or treating
CC   diseases or disorders involving TGF beta e.g., hepatitis. To illustrate
CC   the invention, Selected Interacting Domains (SID) of proteins and their
CC   coding sequences were isolated (ADC64243-ADC64318). The present sequence
CC   was used to illustrate the invention.
XX
SQ   Sequence 780 AA;

  Query Match             29.2%;  Score 709;  DB 7;  Length 780;
  Best Local Similarity   40.7%;  Pred. No. 5.5e-58;
  Matches  143;  Conservative   66;  Mismatches  116;  Indels   26;  Gaps    7;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :    | :|  ::  |  :: : :  |  | : |||:|||||
Db          8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|     ||||| |||:|| |  ||:|||||| :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:|||| | |||:|||||    ::|:    | |:  :::    |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:   |: |     |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :||:|   ||    |
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        303 YQNIKENCAPLYDDALFLRTPQALLAI---------PRPPGGVLRSISVPG 344
                    : |    : |  : :|         |:||    ||  | |
Db        305 ------GAQKIADGVNEINTENMISSIEPEKQDSPPPKPPR--TRSCLVEG 347


RESULT 15
ADL16222
ID   ADL16222 standard; protein; 780 AA.
XX
AC   ADL16222;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human protein tyrosine phosphatase #24.
XX
KW   cytostatic; immunosuppressive; antiallergic;
KW   protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW   inducible signalling pathway; cell proliferation; cancer;
KW   guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW   cell-cycle abnormality; enzyme.
XX
OS   Homo sapiens.
```

XX
PN WO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
PR 12-FEB-2003; 2003US-00366547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
DR N-PSDB; ADL16221.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 71; 238pp; English.
XX
CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (i)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (II) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (III), where
CC dephosphorylation indicates that an active PTP is present. . No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune diseases; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
SQ Sequence 780 AA;

Query Match 29.2%; Score 709; DB 7; Length 780;
Best Local Similarity 40.7%; Pred. No. 5.5e-58;
Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;

```
Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :    | :|  ::  |  :: : :  |  | : |||:|||||
Db          8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:|||||| :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:||||| | |||:|||||    ::|:    | |:  :::    |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:   |: |      |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :||:|   ||    |
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        303 YQNIKENCAPLYDDALFLRTPQALLAI---------PRPPGGVLRSISVPG 344
                      : |    : |   : :|          |:||    ||  | |
Db        305 ------GAQKIADGVNEINTENMISSIEPEKQDSPPPKPPR--TRSCLVEG 347
```

Search completed: December 7, 2004, 09:49:35
Job time : 76 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:48:18 ; Search time 39 Seconds
(without alignments)
778.811 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 2424
Sequence: 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1778.5	73.4	453	3	US-08-821-278A-2	Sequence 2, Appli
2	1754.5	72.4	453	3	US-08-951-260A-7	Sequence 7, Appli
3	1754.5	72.4	453	4	US-09-430-626A-7	Sequence 7, Appli
4	1754.5	72.4	453	4	US-10-243-687-7	Sequence 7, Appli
5	830	34.2	155	3	US-08-821-278A-17	Sequence 17, Appl
6	755.5	31.2	802	3	US-09-081-345-18	Sequence 18, Appl
7	727.5	30.0	807	3	US-09-081-345-2	Sequence 2, Appli
8	715.5	29.5	278	3	US-08-821-278A-18	Sequence 18, Appl
9	695	28.7	272	3	US-08-821-278A-19	Sequence 19, Appl
10	665	27.4	253	2	US-08-685-992-20	Sequence 20, Appl
11	665	27.4	253	2	US-09-144-925-20	Sequence 20, Appl
12	493.5	20.4	255	2	US-08-685-992-16	Sequence 16, Appl
13	493.5	20.4	255	2	US-09-144-925-16	Sequence 16, Appl
14	474	19.6	1711	2	US-08-342-930-2	Sequence 2, Appli
15	467	19.3	595	1	US-08-202-389-6	Sequence 6, Appli
16	465	19.2	631	1	US-08-202-389-8	Sequence 8, Appli
17	463.5	19.1	277	2	US-08-685-992-22	Sequence 22, Appl
18	463.5	19.1	277	2	US-09-144-925-22	Sequence 22, Appl
19	463.5	19.1	513	1	US-08-202-389-2	Sequence 2, Appli
20	463	19.1	843	4	US-09-417-197-117	Sequence 117, App
21	463	19.1	853	4	US-09-417-197-119	Sequence 119, App
22	461	19.0	593	1	US-08-018-129-5	Sequence 5, Appli
23	461	19.0	593	2	US-08-448-250-5	Sequence 5, Appli
24	461	19.0	593	4	US-09-282-257-5	Sequence 5, Appli
25	456	18.8	263	2	US-08-685-992-13	Sequence 13, Appl
26	456	18.8	263	2	US-09-144-925-13	Sequence 13, Appl
27	454	18.7	266	2	US-08-685-992-12	Sequence 12, Appl
28	454	18.7	266	2	US-09-144-925-12	Sequence 12, Appl
29	453	18.7	593	1	US-08-202-389-12	Sequence 12, Appl
30	448.5	18.5	232	2	US-08-446-345-38	Sequence 38, Appl
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32	441.5	18.2	242	2	US-08-685-992-21	Sequence 21, Appl
33	441.5	18.2	242	2	US-09-144-925-21	Sequence 21, Appl
34	435	17.9	1337	3	US-08-854-585-2	Sequence 2, Appli
35	435	17.9	1337	4	US-09-447-533-2	Sequence 2, Appli
36	435	17.9	1337	5	PCT-US95-05512-2	Sequence 2, Appli
37	433	17.9	244	4	US-09-848-294-7	Sequence 7, Appli
38	429.5	17.7	278	1	US-08-201-697-16	Sequence 16, Appl
39	429	17.7	231	2	US-08-446-345-37	Sequence 37, Appl
40	427	17.6	566	4	US-09-270-767-57745	Sequence 57745, A
41	427	17.6	823	4	US-09-270-767-42450	Sequence 42450, A
42	426.5	17.6	802	1	US-08-015-985-1	Sequence 1, Appli
43	426.5	17.6	802	4	US-09-280-597-1	Sequence 1, Appli
44	426	17.6	258	2	US-08-685-992-19	Sequence 19, Appl
45	426	17.6	258	2	US-09-144-925-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-821-278A-2
; Sequence 2, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Mus Musculus
US-08-821-278A-2

Query Match 73.4%; Score 1778.5; DB 3; Length 453;
Best Local Similarity 74.9%; Pred. No. 9.2e-154;
Matches 344; Conservative 32; Mismatches 76; Indels 7; Gaps 2;

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Db          1 MSRHTDLVRSFLEQLEARDYREGAIFVREFSDIKARSVAWKSEGVCSTKAGSRLGNTNKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
              |||||: ||:|||||||||||||| :||| |||||:||| ||||||||||||||||||||
Db         61 RYKDVVAYDETRVILSLLQEEGHGNYINANFIRGIDGSQAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
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Db        121 EFGVKVILMACQETENGRRKCERYWAREQEPLKAGPFCITLTKETTLNADITLRTLQVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
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Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              |||||||||||  |||:|||| |||:|||||||||||||||||||||||:|  |||: |
Db        241 AVDYVRQLLLTQTIPPNFSLFQVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQDTS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
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Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
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RESULT 2
US-08-951-260A-7
; Sequence 7, Application US/08951260A
; Patent No. 6004791
;  GENERAL INFORMATION:
;    APPLICANT:  Aoki, Naohito
;    APPLICANT:  Ullrich, Axel
;    TITLE OF INVENTION:  PROTEIN TYROSINE PHOSPHATASE PTP20
;    TITLE OF INVENTION:  AND RELATED PRODUCTS AND METHODS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/951,260A
;      FILING DATE:  October 16, 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/030,860
;      FILING DATE:  No. 6004791ember 13, 1996
;      APPLICATION NUMBER:  PCT/1897/00946
;      FILING DATE:  June 17, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  227/004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-951-260A-7

  Query Match             72.4%;  Score 1754.5;  DB 3;  Length 453;
  Best Local Similarity   74.5%;  Pred. No. 1.4e-151;
  Matches  342;  Conservative   37;  Mismatches   73;  Indels    7;  Gaps    3;

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Db          1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAWKTEGVCSTKAGSQQGNSKKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
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Db         61 RYKDVVPYDETRVILSLLQEEGHGDYINANFIRGTDGSQAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
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Db        121 EFGIKVILMACQETENGRRKCERYWAQEREPLQAGPFCITLTKETALTSDITLRTLQVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
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Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              |||||||||||| |||:||||:|||:|||||||||||||||||||||:|  |||| |
Db        241 AVDYVRQLLLTQTIPPNFSLFEVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQNNS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
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Db        301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLRSISVPGPPTLPMADTYAVVQKR 360

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Db        361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTENAQGTTALGRVPADENPS 414

Qy        420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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RESULT 3
US-09-430-626A-7
; Sequence 7, Application US/09430626A
; Patent No. 6482605
;   GENERAL INFORMATION:
;        APPLICANT: Aoki, Naohito
;                   Ullrich, Axel
;        TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
;                            AND RELATED PRODUCTS AND METHODS
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/430,626A
;             FILING DATE: 29-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/951,260
;             FILING DATE: October 16, 1997
;             APPLICATION NUMBER: 60/030,860
;             FILING DATE: No. 6482605ember 13, 1996
;             APPLICATION NUMBER: PCT/1897/00946
;             FILING DATE: June 17, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 227/004
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 453 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-430-626A-7

  Query Match             72.4%;  Score 1754.5;  DB 4;  Length 453;
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  Best Local Similarity   74.5%;  Pred. No. 1.4e-151;
  Matches  342;  Conservative   37;  Mismatches   73;  Indels    7;  Gaps    3;

Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
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Db          1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAWKTEGVCSTKAGSQQGNSKKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
              |||||:|||:|||||||||||||| |||| ||||| ||| ||||||||||||||||||||
Db         61 RYKDVVPYDETRVILSLLQEEGHGDYINANFIRGTDGSQAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
              |||:|||||||:| |||||::||||||||:|||| | ||||| ||  |  || ||||:|||
Db        121 EFGIKVILMACQETENGRRKCERYWAQEREPLQAGPFCITLTKETALTSDITLRTLQVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
              ||||| |:|||||||| ||||| ||:| |||||| ||| || ||||||||||||||||||
Db        181 QKESRPVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              |||||||||| |||:||||:|||:|||||||||||||||||||||||:|  |||| |
Db        241 AVDYVRQLLLTQTIPPNFSLFEVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQNNS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
              | |||:||| ||:  |:  |||  || |  || |||||||||| |   ||||||  |||
Db        301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLRSISVPGPPTLPMADTYAVVQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
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Db        361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTENAQGTTALGRVPADENPS 414

Qy        420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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Db        415 GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453


RESULT 4
US-10-243-687-7
; Sequence 7, Application US/10243687
; Patent No. 6797501
;   GENERAL INFORMATION:
;        APPLICANT: Aoki, Naohito
;                   Ullrich, Axel
;        TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
;                            AND RELATED PRODUCTS AND METHODS
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/243,687
;             FILING DATE: 16-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/430,626A
;             FILING DATE: 29-Oct-1999
;             APPLICATION NUMBER: 08/951,260
;             FILING DATE: October 16, 1997
;             APPLICATION NUMBER: 60/030,860
;             FILING DATE: No. 6797501ember 13, 1996
;             APPLICATION NUMBER: PCT/1897/00946
;             FILING DATE: June 17, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 227/004
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 453 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-243-687-7

  Query Match           72.4%;  Score 1754.5;  DB 4;  Length 453;
  Best Local Similarity   74.5%;  Pred. No. 1.4e-151;
  Matches  342;  Conservative   37;  Mismatches   73;  Indels    7;  Gaps    3;

Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
              |||  |  |||||: |||  |:||:|| |||||:| | ||| :||||| |||:  | :||
Db          1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAWKTEGVCSTKAGSQQGNSKKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
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Db         61 RYKDVVPYDETRVILSLLQEEGHGDYINANFIRGTDGSQAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
              |||:|||||||:| |||||::||||||||:|||| | ||||| ||  |  || ||||:|||
Db        121 EFGIKVILMACQETENGRRKCERYWAQEREPLQAGPFCITLTKETALTSDITLRTLQVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
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Db        181 QKESRPVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              |||||||||| |||:||||:|||:|||||||||||||||||||||||:|  |||| |
Db        241 AVDYVRQLLLTQTIPPNFSLFEVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQNNS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
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Db        301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLRSISVPGPPTLPMADTYAVVQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
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Db        361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTENAQGTTALGRVPADENPS 414

Qy        420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |  |||:|  ||||||||||||||||||||||||||||
Db        415 GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453


RESULT 5
US-08-821-278A-17
; Sequence 17, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
;  APPLICANT:  Cheng, Jill
;  APPLICANT:  Lasky, Laurence A.
;  TITLE OF INVENTION:  Protein Tyrosine Phosphatases
;  FILE REFERENCE:  P1010R1
;  CURRENT APPLICATION NUMBER: US/08/821,278A
;  CURRENT FILING DATE:  1997-03-20
;  NUMBER OF SEQ ID NOS:  23
; SEQ ID NO 17
;   LENGTH: 155
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-08-821-278A-17
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  Query Match             34.2%;  Score 830;  DB 3;  Length 155;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-68;
  Matches  155;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 60

Qy         77 LLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIEN 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIEN 120

Qy        137 GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 171
              ||||||||||||||||||||||||||||||||||
Db        121 GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 155


RESULT 6
US-09-081-345-18
; Sequence 18, Application US/09081345
; Patent No. 6228641
;  GENERAL INFORMATION:
;    APPLICANT:  Bahija Jallal
;    APPLICANT:  Gregory D. Plowman
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF
;    TITLE OF INVENTION:  PTP04 RELATED DISORDERS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/081,345
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/047,222
;      FILING DATE:  May 20, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  234/253
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  802 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-081-345-18

  Query Match             31.2%;  Score 755.5;  DB 3;  Length 802;
  Best Local Similarity   44.0%;  Pred. No. 4.4e-60;
  Matches  161;  Conservative   55;  Mismatches  119;  Indels   31;  Gaps    7;

Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :||| :  |    ||:|::||||||:|||| : | ||||  :  | |
Db         25 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || :||:|| |  |||||||||  |||||||:||: : ||:||| | | |:|:||||||
Db         85 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  || | | |:    ||    |  :|||  |  |:| :||  | :|||  |||| |
Db        145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
              :| :: : |  |     |:|:||||||||||:| |||   ||   :|| :||:|:::
Db        204 PILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 263

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325
              :|| |||: |||:|||  :|  | ::|         |  | :|             |  ||
Db        264 EMRTQRPSLVQTQEQYELVYSAVLELF-------KRHMDVISDNHLG--------REIQA 308

Qy        326 LLAIPRPPGGVLRSISVPGS------PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377
              :||       :|::|         | :|| |  |  :  |:|| | :  |:  | |  .
Db        309 QCSIPE------QSLTVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGLRTS 362

Qy        378 ARSAEE 383
              :|||
Db        363 TMNAEE 368


RESULT 7
US-09-081-345-2
; Sequence 2, Application US/09081345
; Patent No. 6228641
;  GENERAL INFORMATION:
;    APPLICANT:  Bahija Jallal
;    APPLICANT:  Gregory D. Plowman
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF
;    TITLE OF INVENTION:  PTP04 RELATED DISORDERS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/081,345
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/047,222
;      FILING DATE:  May 20, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  234/253
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  807 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-081-345-2
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Query Match 30.0%; Score 727.5; DB 3; Length 807;
Best Local Similarity 46.9%; Pred. No. 1.6e-57;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;

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Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :|||    |    :|:|::||||||:|||| :|| |||:  :  | |
Db         25 ANEFLKLKRQSTKYKADKTYPTTVAEKPKNIKKNRYKDILPYDYSRVELSLITSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || |||:|| |  |||||||||  |||||||:||: | :|:||| | | |:|:|||||
Db         85 INANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  |: | | ::   ||    | ::|||| |  |:|::||  | :|||  |||| |
Db        145 EPGEMQLEFGPFSVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
               :| :: : |  |     |:|:|||||||||||:| :||    ||   :|| :||:| ::
Db        204 PILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIDYTWMLLKDGIIPENFSVFSLIR 263

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
              :|| |||: |||:|||  :|: | ::|      :::     ::  ::| |
Db        264 EMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKHSGTESQAKHCIP 313
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RESULT 8
US-08-821-278A-18
; Sequence 18, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-18

Query Match 29.5%; Score 715.5; DB 3; Length 278;
Best Local Similarity 48.9%; Pred. No. 4.3e-57;
Matches 139; Conservative 45; Mismatches 91; Indels 9; Gaps 3;

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Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :||| :  |    ||:|::||||||:|||| : | ||||  :  | |
Db          2 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 61

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || :||:|| |  |||||||||  |||||||::||: : ||:||| | | |:|:|||||
Db         62 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKCERYWA 121

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  || | | |:   ||    |  :||||  |  |:| :||  | :|||  |||| |
Db        122 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 180

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
               :| :: : |  |     |:|:|||||||||||:| |||    ||   :|| :||:|:::
Db        181 PILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 240

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKEN 309
              :|| |||: |||:|||  :|  | ::|         |   | :|
Db        241 EMRTQRPSLVQTQEQYELVYSAVLELF-------KRHMDVISDN 277
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RESULT 9
US-08-821-278A-19
; Sequence 19, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 19
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-19

Query Match 28.7%; Score 695; DB 3; Length 272;
Best Local Similarity 47.1%; Pred. No. 3.1e-55;
Matches 128; Conservative 55; Mismatches 87; Indels 2; Gaps 2;

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Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | :|  ::  |  :: : :  |  | : |||:|||||:|:|:| :|| |:|      |||
Db          2 ARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYKDILPFDHSRVKLTLKTPSQDSDY 61

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYW- 145
              || |||:|| |  ||:|||||| :|::||||:|||: | :|:|||| | |||:|||||
Db         62 INANFIKGVYGPKAYVATQGPLANTVIDFWRMVWEYNVVIIVMACREFEMGRKKCERYWP 121

Qy        146 AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
               ::|:    | |:  :::    |  :||| : || ||| :||  |::|||  |||| |
Db        122 LYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQNESRRLYQFHYVNWPDHDVPSSFD 180

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
               :| |:   |: |     |:|:|||||||||| :| :||   ||    || :|::|:::
Db        181 SILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEEFNVFNLIQ 240

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ 297
              :|| || :||||:|||  ::  :||:|   ||
Db        241 EMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQ 272
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RESULT 10
US-08-685-992-20
; Sequence 20, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240

```
;       TELEFAX:  781-861-9540
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  253 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-685-992-20

  Query Match             27.4%;  Score 665;  DB 2;  Length 253;
  Best Local Similarity   49.4%;  Pred. No. 1.5e-52;
  Matches  126;  Conservative   44;  Mismatches   73;  Indels   12;  Gaps    3;

Qy         48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGP 107
              |  | : |||:||||||:||:| :|| |:|      |||| |||:|| |  ||:|||||
Db          4 TATGEKEENVKKNRYKDILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGP 63

Qy        108 LPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKW 166
              | :|::||||:|||: | :|:|||| | |||:||||    ::|:    | |:
Db         64 LANTVIDFWRMVWEYNVVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISC----- 118

Qy        167 LNEDIMLRT----LKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGP 222
                ||   ||    | : || ||| :||  |::|||  |||| | :| |:    |: |
Db        119 --EDEQARTDYFILLLEFQNESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHED 176

Qy        223 EPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYR 282
              |:|:||||||||||| :| :||   ||    || :|::|::: :|| || :||||:|||
Db        177 VPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYE 236

Qy        283 FLYHTVAQMFCSTLQ 297
               ::  :||:|   ||
Db        237 LVHRAIAQLFEKQLQ 251


RESULT 11
US-09-144-925-20
; Sequence 20, Application US/09144925
; Patent No. 5951979
;  GENERAL INFORMATION:
;    APPLICANT:  Tonks, Nicholas
;    APPLICANT:  Flint, Andrew J.
;    TITLE OF INVENTION:  SUBSTRATE TRAPPING PROTEIN
;    TITLE OF INVENTION:  TYROSINE PHOSPHATASES
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02421-4799
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/144,925
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/685,992
;      FILING DATE:  July 25, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL96-03Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  253 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-144-925-20

  Query Match             27.4%;  Score 665;  DB 2;  Length 253;
  Best Local Similarity   49.4%;  Pred. No. 1.5e-52;
  Matches  126;  Conservative   44;  Mismatches   73;  Indels   12;  Gaps    3;

Qy         48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGP 107
              |  | : |||:||||||:||:| :|| |:|      |||| |||:|| |  ||:|||||
Db          4 TATGEKEENVKKNRYKDILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGP 63

Qy        108 LPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKW 166
              | :|::||||:|||: | :|:|||| | |||:||||    ::|:    | |:
Db         64 LANTVIDFWRMVWEYNVVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISC----- 118

Qy        167 LNEDIMLRT----LKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGP 222
                ||   ||    | : || ||| :||  |::|||  |||| | :| |:    |: |
Db        119 --EDEQARTDYFILLLEFQNESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHED 176

Qy        223 EPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYR 282
              |:|:||||||||||| :| :||   ||    || :|::|::: :|| || :||||:|||
Db        177 VPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYE 236

Qy        283 FLYHTVAQMFCSTLQ 297
               ::  :||:|   ||
Db        237 LVHRAIAQLFEKQLQ 251


RESULT 12
US-08-685-992-16
; Sequence 16, Application US/08685992
; Patent No. 5912138
;  GENERAL INFORMATION:
;    APPLICANT:  Tonks, Nicholas
;    APPLICANT:  Flint, Andrew J.
;    TITLE OF INVENTION:  SUBSTRATE TRAPPING PROTEIN
;    TITLE OF INVENTION:  TYROSINE PHOSPHATASES
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/685,992
;      FILING DATE:  25-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL96-03
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  255 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-685-992-16

  Query Match             20.4%;  Score 493.5;  DB 2;  Length 255;
  Best Local Similarity   43.6%;  Pred. No. 6.8e-37;
  Matches  115;  Conservative   36;  Mismatches   94;  Indels   19;  Gaps    7;

Qy         47 STVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQG 106
              |  :  |   ||   ||||::|||||  :||  |   :  ||   |||||  :|:  |:      :|||||
Db          3 SQMVASASENNAKNRYRNVLPYDWSRVPLKPIHEEPGSDYINASFMPGLWSPQEFIATQG 62

Qy        107 PLPHTLLDFWRLVWEPGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKW 166
              |||  |:  ||||||||       ::|     :|  ||  :||  ||   :  :|     |    :||:  |:
Db         63 PLPQTVGDFWRLVWEQQSHTLVMLTNCMEAGRVKCEHYWPLDSQPCTHGHLRVTLVGEEV 122

Qy        167 LNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARR-----LQGSG 221
              :     :|   |:|   ||  :  ||  |   |  :|||  |||||||  :||       |:       ::|
Db        123 MENWTVLLLLQVEEQK-TLSVRQFHYQAWPDHGVPSSPDTLLAFWRMLRQWLDQTMEGGP 181

Qy        222 PEPLCVHCSAGCGRTGVLCTVD-YVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQ 280
              |     ||||||  ||||  |   :|  :|||      ::  |     |   |  |||:  ||   ||||  |
Db        182 P---IVHCSAGVGRTGTLIALDVLLRQLQSEGLLGP----FSFVRKMRESRPLMVQTEAQ 234

Qy        281 YRFLYHTVAQMFCSTLQNASPHYQ 304
              |  ||:      |   |  :   |:  |   |
Db        235 YVFLH----QCICGS-SNSQPRPQ 253


RESULT 13
US-09-144-925-16
; Sequence 16, Application US/09144925
; Patent No. 5951979
;  GENERAL INFORMATION:
;    APPLICANT:  Tonks, Nicholas
;    APPLICANT:  Flint, Andrew J.
;    TITLE OF INVENTION:  SUBSTRATE TRAPPING PROTEIN
;    TITLE OF INVENTION:  TYROSINE PHOSPHATASES
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02421-4799
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/144,925
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/685,992
;      FILING DATE:  July 25, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL96-03Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  255 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-144-925-16

  Query Match             20.4%;  Score 493.5;  DB 2;  Length 255;
  Best Local Similarity   43.6%;  Pred. No. 6.8e-37;
  Matches  115;  Conservative   36;  Mismatches   94;  Indels   19;  Gaps    7;

Qy         47 STVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQG 106
              |  :  |   ||   ||||::|||||  :||  |   :  ||   |||||  :|:  |:      :|||||
Db          3 SQMVASASENNAKNRYRNVLPYDWSRVPLKPIHEEPGSDYINASFMPGLWSPQEFIATQG 62

Qy        107 PLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKW 166
              |||  |:  ||||||||       ::|     :|  ||  :||  ||   :  :|     |    :||:  |:
Db         63 PLPQTVGDFWRLVWEQQSHTLVMLTNCMEAGRVKCEHYWPLDSQPCTHGHLRVTLVGEEV 122

Qy        167 LNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARR-----LQGSG 221
              :     :|   |:|   ||  :  ||  |   |  :|||  |||||||  :||       |:       ::|
Db        123 MENWTVLLLLQVEEQK-TLSVRQFHYQAWPDHGVPSSPDTLLAFWRMLRQWLDQTMEGGP 181

Qy        222 PEPLCVHCSAGCGRTGVLCTVD-YVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQ 280
              |     ||||||  ||||  |   :|  :|||      ::  |     |   |  |||:  ||   ||||  |
Db        182 P---IVHCSAGVGRTGTLIALDVLLRQLQSEGLLGP----FSFVRKMRESRPLMVQTEAQ 234

Qy        281 YRFLYHTVAQMFCSTLQNASPHYQ 304
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Db        235 YVFLH----QCICGS-SNSQPRPQ 253


RESULT 14
US-08-342-930-2
; Sequence 2, Application US/08342930
; Patent No. 5821084
;  GENERAL INFORMATION:
;    APPLICANT:  OLMSTED, ELIZABETH A.
;    APPLICANT:  MAURO, LAURA J.
;    APPLICANT:  DAVIS, ALAN R.
;    APPLICANT:  DIXON, JACK E.
;    TITLE OF INVENTION:  OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
;    TITLE OF INVENTION:  PHOSPHATASE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/342,930
;      FILING DATE:  21-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KONSKI, ANTOINETTE F.
;      REGISTRATION NUMBER:  34,202
;      REFERENCE/DOCKET NUMBER:  20344-20975.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1711 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-342-930-2
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  Query Match             19.6%;  Score 474;  DB 2;  Length 1711;
  Best Local Similarity   39.9%;  Pred. No. 6.2e-34;
  Matches  114;  Conservative   35;  Mismatches  111;  Indels   26;  Gaps    8;

Qy         10 SFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYD 69
Db       1134 SFRQSYEAKSAHAHQTFFQEFEELKEVGKDQ------PRLEAEHPDNIIKNRYPHVLPYD 1187

Qy         70 QTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILM 129
Db       1188 HSRVRLTQLPGEPHSDYINANFIPGYSHTQEIIATQGPLKKTLEDFWRLVWEQQVHVIIM 1247

Qy        130 ACREIENGRKRCERYWAQEQEPLQTGLFCITLIKE----KWLNEDIMLRTLKVTFQKESR 185
Db       1248 LTVGMENGRVLCEHYWPANSTPVTHGHITIHLLAEEPEDEWTRREFQLQ--HGTEQKQ-R 1304

Qy        186 SVYQLQYMSWPDRGVPSSPDHMLAMV----EEARRLQGSGPEPLCVHCSAGCGRTGVLCT 241
Db       1305 RVKQLQFTTWPDHSVPEAPSSLLAFVELVQEQVQATQGKG--PILVHCSAGVGRTGT--- 1359

Qy        242 VDYVRQLLLTQMIPPD--FSLFDVVLKMRKQRPAAVQTEEQYRFLY 285
Db       1360 --FVALLRLLRQLEEEKVADVFNTVYILRLHRPLMIQTLSQYIFLH 1403


RESULT 15
US-08-202-389-6
; Sequence 6, Application US/08202389
; Patent No. 5536636
;  GENERAL INFORMATION:
;    APPLICANT:  Freeman Jr., Robert M.
;    APPLICANT:  Plutzky, Jorge
;    APPLICANT:  Neel, Benjamin G.
;    APPLICANT:  Rosenberg, Robert D.
;    TITLE OF INVENTION:  IDENTIFICATION OF NOVEL TYROSINE
;    TITLE OF INVENTION:  PHOSPHATASES HAVING SH2 DOMAINS
;    NUMBER OF SEQUENCES:  54
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,389
;      FILING DATE:  28-FEB-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/983,926
;      FILING DATE:  01-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/829,141
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/721,112
;      FILING DATE:  26-JUN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  BIH92-05MA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  595 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-202-389-6

  Query Match             19.3%;  Score 467;  DB 1;  Length 595;
  Best Local Similarity   32.9%;  Pred. No. 6e-34;
  Matches  112;  Conservative   57;  Mismatches  109;  Indels   62;  Gaps   10;

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Db       237 EDTAKAGFWEEFESLQ----KQEVKNLHQRLEGQRPENKGKNRYKNILPFDHSRVIL--- 289

Qy         79 QEEGH------SDYINGNFIRGV-----DGSLAYIATQGPLPHTLLDFWRLVWEFGVKVI 127
Db       290 --QGRDSNIPGSDYINANYIKNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVI 347

Qy        128 LMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKES--- 184
Db       348 VMTTREVEKGRNKCVPYWPEVGMQRAYGPYSVTNVGEHDTTE-YKLRTLQVSPLDNGDLI 406

Qy        185 RSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPE--PLCVHCSAGCGRTGVLCTV 242
Db       407 REIWHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVI 466

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCST------- 295
Db       467 DMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVL 526

Qy        296 ------------------LQNA--------SPHYQNIKEN 309
Db       527 QSQKGQESEYGNITYPPAMKNAHAKASRTSSKHKEDVYEN 566


Search completed: December  7, 2004, 09:54:25
Job time : 41 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:48:18 ; Search time 61 Seconds
(without alignments)
2677.715 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 2424
Sequence: 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582225 seqs, 356638895 residues

Total number of hits satisfying chosen parameters: 1582225

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2424	100.0	458	13	US-10-087-993-36	Sequence 36, Appl
2	1754.5	72.4	453	14	US-10-243-687-7	Sequence 7, Appli
3	1724.5	71.1	448	13	US-10-087-993-32	Sequence 32, Appl
4	755.5	31.2	802	9	US-09-822-295-18	Sequence 18, Appl
5	755.5	31.2	802	14	US-10-366-547-95	Sequence 95, Appl
6	755.5	31.2	802	15	US-10-309-423-5	Sequence 5, Appli
7	727.5	30.0	807	9	US-09-822-295-2	Sequence 2, Appli
8	709	29.2	780	14	US-10-366-547-69	Sequence 69, Appl
9	709	29.2	780	14	US-10-366-547-71	Sequence 71, Appl
10	708	29.2	692	15	US-10-309-423-4	Sequence 4, Appli
11	708	29.2	778	16	US-10-322-281-848	Sequence 848, App
12	708	29.2	808	15	US-10-309-423-2	Sequence 2, Appli
13	706	29.1	773	16	US-10-322-281-845	Sequence 845, App
14	705.5	29.1	382	14	US-10-366-547-77	Sequence 77, Appl
15	703	29.0	775	14	US-10-366-547-75	Sequence 75, Appl
16	665	27.4	312	9	US-09-788-626-21	Sequence 21, Appl
17	523	21.6	235	15	US-10-087-684-94	Sequence 94, Appl
18	523	21.6	235	15	US-10-218-779-94	Sequence 94, Appl
19	523	21.6	235	15	US-10-072-012-819	Sequence 819, App
20	521.5	21.5	263	15	US-10-087-684-93	Sequence 93, Appl
21	521.5	21.5	263	15	US-10-218-779-93	Sequence 93, Appl
22	496.5	20.5	264	14	US-10-245-539-6	Sequence 6, Appli
23	493.5	20.4	313	9	US-09-788-626-17	Sequence 17, Appl
24	491.5	20.3	1093	14	US-10-245-539-4	Sequence 4, Appli
25	491.5	20.3	1118	14	US-10-245-539-2	Sequence 2, Appli
26	491.5	20.3	1118	14	US-10-245-539-8	Sequence 8, Appli
27	482.5	19.9	613	14	US-10-366-547-97	Sequence 97, Appl
28	463.5	19.1	341	9	US-09-788-626-23	Sequence 23, Appl
29	463	19.1	595	9	US-09-920-021A-1	Sequence 1, Appli
30	463	19.1	595	14	US-10-366-547-87	Sequence 87, Appl
31	463	19.1	595	14	US-10-366-547-91	Sequence 91, Appl
32	463	19.1	597	14	US-10-366-547-89	Sequence 89, Appl
33	463	19.1	621	15	US-10-264-049-3086	Sequence 3086, Ap
34	463	19.1	843	14	US-10-072-036-117	Sequence 117, App
35	463	19.1	853	14	US-10-072-036-119	Sequence 119, App
36	458	18.9	593	14	US-10-262-552-2	Sequence 2, Appli
37	458	18.9	593	14	US-10-366-547-26	Sequence 26, Appl
38	458	18.9	593	16	US-10-703-210-2	Sequence 2, Appli
39	456	18.8	322	9	US-09-788-626-14	Sequence 14, Appl
40	454	18.7	325	9	US-09-788-626-13	Sequence 13, Appl
41	453	18.7	593	9	US-09-920-021A-3	Sequence 3, Appli
42	453	18.7	593	14	US-10-366-547-28	Sequence 28, Appl
43	453	18.7	593	14	US-10-366-547-30	Sequence 30, Appl
44	453	18.7	593	14	US-10-366-547-32	Sequence 32, Appl
45	453	18.7	593	15	US-10-444-795B-789	Sequence 789, App

ALIGNMENTS

RESULT 1
US-10-087-993-36
; Sequence 36, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Naylor, Oliver
; Kharitonenkov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
; AND SIRP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150

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;              FILING DATE: June 17, 1997
;              APPLICATION NUMBER: U.S. 60/019,629
;              FILING DATE: June 17, 1996
;              APPLICATION NUMBER: U.S. 60/023,485
;              FILING DATE: August 9, 1996
;              APPLICATION NUMBER: U.S. 60/030,860
;              FILING DATE: No. US20020169303A1ember 13, 1996
;              APPLICATION NUMBER: U.S. 60/034,286
;              FILING DATE: December 19, 1996
;              APPLICATION NUMBER: U.S. 60/030,964
;              FILING DATE: No. US20020169303A1ember 15, 1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Warburg, Richard J.
;              REGISTRATION NUMBER: 32,327
;              REFERENCE/DOCKET NUMBER: 225/298
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (213) 489-1600
;              TELEFAX: (213) 955-0440
;              TELEX: 67-3510
;    INFORMATION FOR SEQ ID NO: 36:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 458 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: peptide
;         SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-087-993-36

  Query Match             100.0%;  Score 2424;  DB 13;  Length 458;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-189;
  Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
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Db          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
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Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
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Db        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
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Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
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Db        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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Db        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458


RESULT 2
US-10-243-687-7
; Sequence 7, Application US/10243687
; Publication No. US20030073120A1
;   GENERAL INFORMATION:
;        APPLICANT: Aoki, Naohito
;                   Ullrich, Axel
;        TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
;                            AND RELATED PRODUCTS AND METHODS
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/243,687
;             FILING DATE: 16-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/430,626A
;             FILING DATE: 29-Oct-1999
;             APPLICATION NUMBER: 08/951,260
;             FILING DATE: October 16, 1997
;             APPLICATION NUMBER: 60/030,860
;             FILING DATE: No. US20030073120A1ember 13, 1996
;             APPLICATION NUMBER: PCT/1897/00946
;             FILING DATE: June 17, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 227/004
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;    INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 453 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
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US-10-243-687-7

  Query Match             72.4%;  Score 1754.5;  DB 14;  Length 453;
  Best Local Similarity   74.5%;  Pred. No. 1.3e-134;
  Matches  342;  Conservative   37;  Mismatches   73;  Indels    7;  Gaps    3;

Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
              |||  |  |||||: |||  |:||:|| |||||:| | ||| :||||| |||:  | :||
Db          1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAWKTEGVCSTKAGSQQGNSKKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
              |||||:|||:|||||||||||||| |||| ||||| ||| ||||||||||||||||||||
Db         61 RYKDVVPYDETRVILSLLQEEGHGDYINANFIRGTDGSQAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
              |||:|||||||:| |||||::|||||||:|||| | ||||| ||  |  || ||||:|||
Db        121 EFGIKVILMACQETENGRRKCERYWAQEREPLQAGPFCITLTKETALTSDITLRTLQVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
              ||||| |:|||||||||| ||||| ||:| |||||| ||| || ||||||||||||||||
Db        181 QKESRPVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              |||||||||||| |||:||||:|||:|||||||||||||||||||||||:|  |||| |
Db        241 AVDYVRQLLLTQTIPPNFSLFEVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQNNS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
```

```
Db        301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLRSISVPGPPTLPMADTYAVVQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
Db        361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTENAQGTTALGRVPADENPS 414

Qy        420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
Db        415 GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453


RESULT 3
US-10-087-993-32
; Sequence 32, Application US/10087993
; Publication No. US20020169303A1
;   GENERAL INFORMATION:
;        APPLICANT: Ullrich, Axel
;                   Aoki, Naohito
;                   Kim, Yeong Woong
;                   Wang, Hong Yang
;                   Chen, Zhengjun
;                   Naylor, Oliver
;                   Kharitonenkov, Alexei Igorevich
;        TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
;                            AND SIRP POLYPEPTIDES AND RELATED
;                            PRODUCTS AND METHODS
;        NUMBER OF SEQUENCES: 38
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/087,993
;             FILING DATE: 05-Mar-2002
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/877,150
;             FILING DATE: June 17, 1997
;             APPLICATION NUMBER: U.S. 60/019,629
;             FILING DATE: June 17, 1996
;             APPLICATION NUMBER: U.S. 60/023,485
;             FILING DATE: August 9, 1996
;             APPLICATION NUMBER: U.S. 60/030,860
;             FILING DATE: No. US20020169303A1ember 13, 1996
;             APPLICATION NUMBER: U.S. 60/034,286
;             FILING DATE: December 19, 1996
;             APPLICATION NUMBER: U.S. 60/030,964
;             FILING DATE: No. US20020169303A1ember 15, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 225/298
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 32:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 453 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-087-993-32

  Query Match             71.1%;  Score 1724.5;  DB 13;  Length 448;
  Best Local Similarity   74.2%;  Pred. No. 3.5e-132;
  Matches  337;  Conservative   37;  Mismatches   73;  Indels    7;  Gaps    3;

Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
Db          1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAWKTEGVCSTKAGSQQGNSKKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
Db         61 RYKDVVPYDETRVILSLLQEEGHGDYINANFIRGTDGSQAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
Db        121 EFGIKVILMACQETENGRRKCERYWAQEREPLQAGPFCITLTKETALTSDITLRTLQVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
Db        181 QKESRPVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
Db        241 AVDYVRQLLLTQTIPPNFSLFEVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQNNS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
Db        301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLRSISVPGPPTLPMADTYAVVQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
Db        361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTENAQGTTALGRVPADENPS 414

Qy        420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPA 453
Db        415 GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPA 448


RESULT 4
US-09-822-295-18
; Sequence 18, Application US/09822295
; Patent No. US20020119501A1
;   GENERAL INFORMATION:
;        APPLICANT: Bahija Jallal
;                   Gregory D. Plowman
;        TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
;                            PTP04 RELATED DISORDERS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/822,295
;             FILING DATE: 02-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/081,345
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
```

```
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 234/253
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 802 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-822-295-18

  Query Match             31.2%;  Score 755.5;  DB 9;  Length 802;
  Best Local Similarity   44.0%;  Pred. No. 1.1e-52;
  Matches  161;  Conservative   55;  Mismatches  119;  Indels   31;  Gaps    7;

Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :||| :  |     ||:|::||||||:|||| : | ||||  :  | |
Db         25 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || :||:|| |  |||||||||  |||||||::||: : ||:||| | | |:|:||||||
Db         85 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  || | | |:   ||    |  :|||| |  |:| :||  | :|||  |||| |
Db        145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
               :| :: : |  |     |:|:||||||||||:| |||   ||   :|| :||:|:::
Db        204 PILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 263

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325
              :|| |||: |||:|||  :|  | ::|          |    | :|              | ||
Db        264 EMRTQRPSLVQTQEQYELVYSAVLELF-------KRHMDVISDNHLG--------REIQA 308

Qy        326 LLAIPRPPGGVLRSISVPGS------PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377
                :||       :|::|         | :|| |  |  :  |:|| | :  |:  |  |
Db        309 QCSIPE------QSLTVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGLRTS 362

Qy        378 ARSAEE 383
                :|||
Db        363 TMNAEE 368


RESULT 5
US-10-366-547-95
; Sequence 95, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
;  APPLICANT: Meng, Tzu-Ching
;  APPLICANT:  Tonks, Nicholas K.
;  APPLICANT:  Cool, Deborah E.
;  TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE: 200125.439
;  CURRENT APPLICATION NUMBER: US/10/366,547
;  CURRENT FILING DATE:  2003-02-12
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
;   LENGTH: 802
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-366-547-95

  Query Match             31.2%;  Score 755.5;  DB 14;  Length 802;
  Best Local Similarity   44.0%;  Pred. No. 1.1e-52;
  Matches  161;  Conservative   55;  Mismatches  119;  Indels   31;  Gaps    7;

Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :||| :  |     ||:|::||||||:|||| : | ||||  :  | |
Db         25 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || :||:|| |  |||||||||  |||||||::||: : ||:||| | | |:|:||||||
Db         85 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  || | | |:   ||    |  :|||| |  |:| :||  | :|||  |||| |
Db        145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
               :| :: : |  |     |:|:||||||||||:| |||   ||   :|| :||:|:::
Db        204 PILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 263

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325
              :|| |||: |||:|||  :|  | ::|          |    | :|              | ||
Db        264 EMRTQRPSLVQTQEQYELVYSAVLELF-------KRHMDVISDNHLG--------REIQA 308

Qy        326 LLAIPRPPGGVLRSISVPGS------PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377
                :||       :|::|         | :|| |  |  :  |:|| | :  |:  |  |
Db        309 QCSIPE------QSLTVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGLRTS 362

Qy        378 ARSAEE 383
                :|||
Db        363 TMNAEE 368


RESULT 6
US-10-309-423-5
; Sequence 5, Application US/10309423
; Publication No. US20040006777A1
; GENERAL INFORMATION:
;  APPLICANT: HSC Research and Development Limited Partnership
;  TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
;  FILE REFERENCE: 92906-2
;  CURRENT APPLICATION NUMBER: US/10/309,423
;  CURRENT FILING DATE:  2002-12-03
;  PRIOR APPLICATION NUMBER: US/09/600,358
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: CA 2,220,853
;  PRIOR FILING DATE: 1998-01-16
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 802
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-309-423-5

  Query Match             31.2%;  Score 755.5;  DB 15;  Length 802;
  Best Local Similarity   44.0%;  Pred. No. 1.1e-52;
  Matches  161;  Conservative   55;  Mismatches  119;  Indels   31;  Gaps    7;

Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :||| :  |     ||:|::||||||:|||| : | ||||  :  | |
Db         25 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || :||:|| |  |||||||||  |||||||::||: : ||:||| | | |:|:||||||
Db         85 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  || | | |:   ||    |  :|||| |  |:| :||  | :|||  |||| |
Db        145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
               :| :: : |  |     |:|:||||||||||:| |||   ||   :|| :||:|:::
Db        204 PILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 263
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Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325
              :|| |||: |||:|||  :|  | ::|          |   | :|            | ||
Db        264 EMRTQRPSLVQTQEQYELVYSAVLELF-------KRHMDVISDNHLG--------REIQA 308

Qy        326 LLAIPRPPGGVLRSISVPGS------PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377
                :||       :|::|         | :|| |  |   :  :|:|| | :  |:  |  |
Db        309 QCSIPE------QSLTVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGLRTS 362

Qy        378 ARSAEE 383
                :|||
Db        363 TMNAEE 368


RESULT 7
US-09-822-295-2
; Sequence 2, Application US/09822295
; Patent No. US20020119501A1
;   GENERAL INFORMATION:
;        APPLICANT: Bahija Jallal
;                   Gregory D. Plowman
;        TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
;                            PTP04 RELATED DISORDERS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/822,295
;             FILING DATE: 02-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/081,345
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 234/253
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 807 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-822-295-2

  Query Match             30.0%;  Score 727.5;  DB 9;  Length 807;
  Best Local Similarity   46.9%;  Pred. No. 2.2e-50;
  Matches  136;  Conservative   56;  Mismatches   93;  Indels    5;  Gaps    3;

Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :|||     |    :|:|::|||||:|||| :|| |||:  :  | |
Db         25 ANEFLKLKRQSTKYKADKTYPTTVAEKPKNIKKNRYKDILPYDYSRVELSLITSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || |||:|| |  |||||||||  |||||||::||: | :|:|||  | | |:|:|||||
Db         85 INANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWA 144


Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  |: | | ::   ||    | ::|||||  |  :|::||   | :|||  |||| |
Db        145 EPGEMQLEFGPFSVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
              :| :: : |  |     |:|:|||||||||||:| :||   ||   :|| :||:| ::
Db        204 PILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIDYTWMLLKDGIIPENFSVFSLIR 263

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
              :|| |||: |||:|||  :|: | ::|      :::     ::  ::| |
Db        264 EMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKHSGTESQAKHCIP 313


RESULT 8
US-10-366-547-69
; Sequence 69, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
;  APPLICANT: Meng, Tzu-Ching
;  APPLICANT:  Tonks, Nicholas K.
;  APPLICANT:  Cool, Deborah E.
;  TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE: 200125.439
;  CURRENT APPLICATION NUMBER: US/10/366,547
;  CURRENT FILING DATE:  2003-02-12
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69
;   LENGTH: 780
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-366-547-69

  Query Match             29.2%;  Score 709;  DB 14;  Length 780;
  Best Local Similarity   41.0%;  Pred. No. 6.9e-49;
  Matches  144;  Conservative   65;  Mismatches  116;  Indels   26;  Gaps    7;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :    | :|  ::  |  :: : :  |  | : |||:|||||
Db          8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:|||||| :|::||||:|||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMVWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:|||||  | |||:|||||    ::|:    | |:  :::    |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:    |: |      |:|:||||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :|||:|   ||    |
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        303 YQNIKENCAPLYDDALFLRTPQALLAI---------PRPPGGVLRSISVPG 344
                      : |   : |  : :|          |:||    ||  | |
Db        305 ------GAQKIADGVNEINTENMVSSIEPEKQDSPPPKPPR--TRSCLVEG 347


RESULT 9
US-10-366-547-71
; Sequence 71, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
;  APPLICANT: Meng, Tzu-Ching
;  APPLICANT:  Tonks, Nicholas K.
;  APPLICANT:  Cool, Deborah E.
;  TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
```

```
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE: 200125.439
;  CURRENT APPLICATION NUMBER: US/10/366,547
;  CURRENT FILING DATE:  2003-02-12
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
;   LENGTH: 780
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-366-547-71

  Query Match             29.2%;  Score 709;  DB 14;  Length 780;
  Best Local Similarity   40.7%;  Pred. No. 6.9e-49;
  Matches  143;  Conservative   66;  Mismatches  116;  Indels   26;  Gaps    7;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :   | :|  ::  |  :: : :  |  | : |||:|||||
Db          8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:||||||  :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:|||||  | |||:||||     ::|:    | |:  :::     |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  ||||  | :|  |:   |: |      |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
              ||    ||    || :|::|::: :|| || :||||:|||  ::  :||:|    ||     |
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        303 YQNIKENCAPLYDDALFLRTPQALLAI---------PRPPGGVLRSISVPG 344
                  : |    : |   : :|         |:||    ||  | |
Db        305 ------GAQKIADGVNEINTENMISSIEPEKQDSPPPKPPR--TRSCLVEG 347


RESULT 10
US-10-309-423-4
; Sequence 4, Application US/10309423
; Publication No. US20040006777A1
; GENERAL INFORMATION:
;  APPLICANT: HSC Research and Development Limited Partnership
;  TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
;  FILE REFERENCE: 92906-2
;  CURRENT APPLICATION NUMBER: US/10/309,423
;  CURRENT FILING DATE:  2002-12-03
;  PRIOR APPLICATION NUMBER: US/09/600,358
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: CA 2,220,853
;  PRIOR FILING DATE: 1998-01-16
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 692
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-423-4

  Query Match             29.2%;  Score 708;  DB 15;  Length 692;
  Best Local Similarity   46.7%;  Pred. No. 7.1e-49;
  Matches  136;  Conservative   54;  Mismatches   95;  Indels    6;  Gaps    4;

Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :|||     |      :|::||||||:|||| :|| |||:  :  | |
Db         25 ANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || |||:|| |  |||||||||  |||||||::||: | :|:||| | | |:|:||||||
Db         85 INANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
              :  |  |: | | ::   ||    | ::||||| |  |:|::||  | :|||  |||| |
Db        145 EPGEMQLEFGPFSVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCT-VDYVRQLLLTQMIPPDFSLFDVV 264
              :| :: : |  |      |:|:||||||||||:|  |||   ||   :|| :||:| ::
Db        204 PILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLI 263

Qy        265 LKMRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
              :|| |||: |||:|||  :|: | ::|      :::     ::  ::| |
Db        264 REMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKHSGTESQAKHCIP 314


RESULT 11
US-10-322-281-848
; Sequence 848, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc S. Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: 529452001000
;  CURRENT APPLICATION NUMBER: US/10/322,281
;  CURRENT FILING DATE:  2002-12-17
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 848
;   LENGTH: 778
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-322-281-848

  Query Match             29.2%;  Score 708;  DB 16;  Length 778;
  Best Local Similarity   40.7%;  Pred. No. 8.3e-49;
  Matches  143;  Conservative   66;  Mismatches  116;  Indels   26;  Gaps    7;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :   | :|  ::  |  :: : :  |  | : |||:|||||
Db          8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:||||||  :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:|||||  | |||:||||     ::|:    | |:  :::     |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  ||||  | :|  |:   |: |      |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
              ||    ||    || :|::|::: :|| || :||||:|||  ::  :||:|    ||     |
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        303 YQNIKENCAPLYDDALFLRTPQALLAI---------PRPPGGVLRSISVPG 344
                  : |    : |   : :|         |:||    ||  | |
Db        305 ------GAQKIADGVNEINTENMVSSIEPEKQDSPPPKPPR--TRSCLVEG 347


RESULT 12
US-10-309-423-2
; Sequence 2, Application US/10309423
; Publication No. US20040006777A1
; GENERAL INFORMATION:
;  APPLICANT: HSC Research and Development Limited Partnership
;  TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
;  FILE REFERENCE: 92906-2
;  CURRENT APPLICATION NUMBER: US/10/309,423
;  CURRENT FILING DATE:  2002-12-03
```

```
;  PRIOR APPLICATION NUMBER: US/09/600,358
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: CA 2,220,853
;  PRIOR FILING DATE: 1998-01-16
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 808
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-309-423-2

  Query Match           29.2%;  Score 708;  DB 15;  Length 808;
  Best Local Similarity  46.7%;  Pred. No. 8.7e-49;
  Matches  136;  Conservative   54;  Mismatches   95;  Indels    6;  Gaps    4;

Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
Db         25 ANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
Db         85 INANFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
Db        145 EPGEMQLEFGPFSVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCT-VDYVRQLLLTQMIPPDFSLFDVV 264
Db        204 PILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLKDGIIPENFSVFSLI 263

Qy        265 LKMRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
Db        264 REMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKHSGTESQAKHCIP 314


RESULT 13
US-10-322-281-845
; Sequence 845, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc S. Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: 529452001000
;  CURRENT APPLICATION NUMBER: US/10/322,281
;  CURRENT FILING DATE:  2002-12-17
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 845
;   LENGTH: 773
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-322-281-845

  Query Match           29.1%;  Score 706;  DB 16;  Length 773;
  Best Local Similarity  25.5%;  Pred. No. 1.2e-48;
  Matches  196;  Conservative   86;  Mismatches  163;  Indels  324;  Gaps   20;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
Db          8 RRFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMF---------- 292
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        293 ----------------------------------C--------STLQNASPH----- 302
Db        305 GAQKIADGNEITTGTMVSSIDSEKQDSPPPKPPRTRSCLVEGDAKEEILQPPEPHPVPPI 364

Qy        303 ------------------------------------------------------------Y 303
Db        365 LTPSPPSAFPTVTTVWQDSDRYHPKPVLHMDEQHPADLNRSYDKSADPMGKSESAIEHID 424

Qy        304 QNIKENCA------PL------YDDALFL----------------RT--PQALLA---- 328
Db        425 KKLERNLSFEIKKVPLQEGPKSFDGNTLLNRGHAIKIKSASSSVVDRTSKPQELSAGALK 484

Qy        329 --------------------------------IPRP-------PGGVLRSI-------S 341
Db        485 VDDVSQNSCADCSAAHSHRAAESSEESQSNSHTPPRPDCLPLDKKGHVTWSLHGPENATP 544

Qy        342 VPGSPGHAMADTY--------------AEEQKR-------------------------- 360
Db        545 VPDSPDGKSPDNHSQTLKTVSSTPNSTAEEEAHDLTEHHNSSPLLKAPLSFTNPLHSDDS 604

Qy        361 ----GAPAGAGSGTQTGTGTGA-----RSAEEAPLYSKVTPR--------------AQRP 397
Db        605 DSDGGSSDGAVTRNKTSISTASATVSPASSAESACTRRVLPMSIARQEVAGTPHSGAEKD 664

Qy        398 GAHAEDARGTLPGRVP------------------------------------------- 413
Db        665 ADVSEESPPPLPERTPESFVLADMPVRPEWHELPNQEWSEQRESEGLTTSGNEKHDAGGI 724

Qy        414 -----ADQSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT 456
Db        725 HTEASADSPPAFSDKKDQITKSPAEVTDIGFGNRCGKPKGPREPPSEWT 773


RESULT 14
US-10-366-547-77
; Sequence 77, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
;  APPLICANT: Meng, Tzu-Ching
;  APPLICANT:  Tonks, Nicholas K.
;  APPLICANT:  Cool, Deborah E.
;  TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE: 200125.439
;  CURRENT APPLICATION NUMBER: US/10/366,547
;  CURRENT FILING DATE:  2003-02-12
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 382
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-366-547-77

  Query Match           29.1%;  Score 705.5;  DB 14;  Length 382;
  Best Local Similarity  45.1%;  Pred. No. 5.1e-49;
  Matches  133;  Conservative   59;  Mismatches   94;  Indels    9;  Gaps    4;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
Db          8 RRFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPRAYVATQGPLANTVIDFWRMIWEYN 125
```

```
Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:||||| | |||:|||||    ::|:    | |:   |:    |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:   |: |     |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ 297
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :||:|   ||
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQ 299


RESULT 15
US-10-366-547-75
; Sequence 75, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
;  APPLICANT: Meng, Tzu-Ching
;  APPLICANT:  Tonks, Nicholas K.
;  APPLICANT:  Cool, Deborah E.
;  TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
;  TITLE OF INVENTION:  PHOSPHATASES
;  FILE REFERENCE: 200125.439
;  CURRENT APPLICATION NUMBER: US/10/366,547
;  CURRENT FILING DATE:  2003-02-12
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
;   LENGTH: 775
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-366-547-75

  Query Match             29.0%;  Score 703;  DB 14;  Length 775;
  Best Local Similarity   25.0%;  Pred. No. 2.1e-48;
  Matches  194;  Conservative   84;  Mismatches  162;  Indels  336;  Gaps   17;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :    | :|  ::  |  :: : :  |  | : |||:|||||
Db          8 RRFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:|||||  :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPFRNTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:||||| | |||:|||||    ::|:    | |:   |:    |  :||| : ||
Db        126 VVMIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:   |: |     |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ----- 297
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :||:|   ||
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        298 ------------------------------------------------------------ 297

Db        305 GAQKIRDGNEITTGTMVSSIDSEKQDSPPPKPPRTRSCLVEGDAKEEILQPPEPHPVPPI 364

Qy        298 ----------------------------NASP--------------------------- 301
                                           |||
Db        365 LTPSPPSAFPTVTTVWQDSDRYHPKPVLHMASPEQHPADLNRSYDKSADQWGKSESAIEH 424

Qy        302 --------------------------------HYQNIKENCAPLYDDALFLRT--PQA 325
                                             |  ||  : : |     ||  ||
Db        425 IDKKLERNLSFEIKKVPLQEGPKSFDGNTLLNRGHAIKIKSASSSVVD-----RTSKPQE 479

Qy        326 LLA-----------------------------------IPRP-------PGGVLRSI- 340
              | |                                   |||       | |  |:
Db        480 LSAGALKVDDVSQNSCADCSAAHSHRAAESSEESQSNSHTPPRPDCLPLDKKGHVTWSLH 539

Qy        341 ------SVPGSPGHAMADTY-------------AEEQKR------------------- 360
                   || ||     | :               |||:
Db        540 GPENATPVPDSPDGKSPDNHSQTLKTVSSTPNSTAEEEAHDLTEHHNSSPLLKAPLSFTN 599

Qy        361 -----------GAPAGAGSGTQTGTGTGA-----RSAEEAPLYSKVTPR----------- 393
                         |:  || :  :|   | :      |: |:  : :| |
Db        600 PLHSDDWHSDGGSSDGAVTRNKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTP 659

Qy        394 ---AQRPGAHAEDARGTLPGRVP------------------------------------ 413
                  |::    :|::   || | |
Db        660 HSGAEKDADVSEESPPPLPERTPESFVLADMPVRPEWHELPNQEWSEQRESEGLTTSGNE 719

Qy        414 ------------ADQSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT 456
                         ||  || |   : :    |:   :||  | |:|||||:||:|||
Db        720 KHDAGGIHTEASADSPPAFSDKKDQITKSPAEVTDIGFGNRCGKPKGPREPPSEWT 775


Search completed: December  7, 2004, 09:55:32
Job time : 63 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:48:13 ; Search time 40 Seconds
(without alignments)
1101.682 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 2424
Sequence: 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	755.5	31.2	802	1	B44390	protein-tyrosine-p
2	710	29.3	773	1	JH0609	protein-tyrosine-p
3	709	29.2	780	1	JC1368	protein-tyrosine-p
4	705.5	29.1	382	1	S48748	protein-tyrosine-p
5	705	29.1	775	2	S55345	protein-tyrosine-p
6	491.5	20.3	1118	1	A49724	protein-tyrosine-p
7	475.5	19.6	595	1	A44390	protein-tyrosine-p
8	474	19.6	1711	1	A55148	protein-tyrosine-p
9	463	19.1	595	1	S20825	protein-tyrosine-p
10	462	19.1	926	1	A41105	protein-tyrosine-p
11	453	18.7	593	1	JN0805	protein-tyrosine-p
12	453	18.7	593	2	JC5167	protein-tyrosine-p
13	451	18.6	585	2	A46209	protein-tyrosine-p
14	449	18.5	597	1	A53593	protein-tyrosine-p
15	448	18.5	521	1	A44267	protein-tyrosine-p
16	448	18.5	913	1	A41109	protein-tyrosine-p
17	444	18.3	595	1	A55651	protein-tyrosine-p
18	442	18.2	694	2	A53978	protein-tyrosine-p
19	441	18.2	597	2	B53978	protein-tyrosine-p
20	435	17.9	1337	1	I38670	protein-tyrosine-p
21	431	17.8	398	2	T08716	protein-tyrosine-p
22	430.5	17.8	435	1	TPHUN1	protein-tyrosine-p
23	430.5	17.8	832	2	JC8051	protein tyrosine p
24	430	17.7	593	1	A42690	protein-tyrosine-p
25	429.5	17.7	583	2	S17671	protein-tyrosine-p
26	428	17.7	624	2	T19630	hypothetical prote
27	428	17.7	1026	2	T19631	protein-tyrosine-p
28	426.5	17.6	802	1	A36065	protein-tyrosine-p
29	424.5	17.5	1437	2	T31093	probable protein-t
30	424.5	17.5	2490	1	A54971	protein-tyrosine-p
31	424	17.5	1301	1	A41622	protein-tyrosine-p
32	423.5	17.5	829	1	A47373	protein-tyrosine-p
33	423	17.5	360	1	JH0692	protein-tyrosine-p
34	421.5	17.4	1238	2	S68700	HPTP beta-like tyr
35	421.5	17.4	2294	2	I67630	protein-tyrosine-p
36	421.5	17.4	2466	2	I67629	protein-tyrosine-p
37	421	17.4	1200	2	T43148	probable protein-t
38	420	17.3	1898	2	S46216	leukocyte antigen-
39	420	17.3	2051	2	T30938	receptor tyrosine
40	419.5	17.3	1188	1	A57064	protein-tyrosine-p
41	419.5	17.3	1216	2	S60613	protein-tyrosine-p
42	419.5	17.3	1997	1	S12050	protein-tyrosine-p
43	419	17.3	1442	1	B48148	protein-tyrosine-p
44	419	17.3	1445	1	A48148	protein-tyrosine-p
45	418.5	17.3	405	2	I49372	protein-tyrosine-p

ALIGNMENTS

RESULT 1
B44390
protein-tyrosine-phosphatase (EC 3.1.3.48) PEP, nonreceptor type 8 - mouse
N;Alternate names: protein-tyrosine-phosphatase PEP
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: B44390; S71952; S27876
R;Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
Mol. Cell. Biol. 12, 2396-2405, 1992
A;Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: c
, and threonine-rich sequences.
A;Reference number: A44390; MUID:92236615; PMID:1373816
A;Accession: B44390
A;Molecule type: mRNA
A;Residues: 1-802 <MAT>
A;Cross-references: UNIPROT:P29352; GB:M90388; NID:g200522; PIDN:AAA39994.1; PID:g200523
R;Cloutier, J.F.; Veillette, A.
EMBO J. 15, 4909-4918, 1996
A;Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosine
A;Reference number: S71952; MUID:97045099; PMID:8890164
A;Accession: S71952
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 495-789 <CLO>
C;Comment: This protein is found primarily in hematopoietic tissues.
C;Genetics:
A;Gene: 70zpep
C;Complex: physically associates with inhibitory tyrosine protein kinase Csk; interactior
C;Function:
A;Description: probably an effector and/or regulator of tyrosine protein kinase csk in T-
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phospha
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;54-278/Domain: protein-tyrosine-phosphatase homology <PTP>
F;497-802/Region: glutamic acid/proline/serine/threonine-rich
F;613-621/Region: proline-rich
F;688-695/Region: proline-rich
F;227/Active site: Cys (phosphocysteine intermediate) #status predicted
F;233/Binding site: substrate phosphate (Arg) #status predicted

Query Match 31.2%; Score 755.5; DB 1; Length 802;
Best Local Similarity 44.0%; Pred. No. 2.9e-47;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

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Qy         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 86
              | ||  ::  |  :||| :  |    ||:|::|||||:|||| : | ||||  :  | |
Db         25 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 84

Qy         87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 146
              || :||:|| |  |||||||||  |||||||::||: : ||:||| | | |:|:||||||
Db         85 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKCERYWA 144

Qy        147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
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           :  |  || | | |:   ||    |  :||||  |  |:| :||  | :|||  |||| |
Db        145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 203

Qy        206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
              :| :: : |  |      |:|:||||||||||:| |||   ||   :|| :||:|:::
Db        204 PILQLIWDMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 263

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325
              :|| |||: |||:|||  :|  | ::|         |  | :|           |  ||
Db        264 EMRTQRPSLVQTQEQYELVYSAVLELF-------KRHMDVISDNHLG--------REIQA 308

Qy        326 LLAIPRPPGGVLRSISVPGS------PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377
                :||       :|::|         | :|| |  |  :  |:|| | :  |:  |  |
Db        309 QCSIPE------QSLTVEADSCPLDLPKNAMRDVKTTNQHSKQGAEAESTGGSSLGLRTS 362

Qy        378 ARSAEE 383
                :|||
Db        363 TMNAEE 368


RESULT 2
JH0609
protein-tyrosine-phosphatase (EC 3.1.3.48) P19 - mouse
N;Alternate names: protein-tyrosine-phosphatase PTPTY43
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JH0609; PS0365; PS0369; PS0366; G61180
R;den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
A;Title: Differential expression of a novel murine non-receptor protein tyrosine phospha
A;Reference number: JH0609; MUID:92272714; PMID:1590786
A;Accession: JH0609
A;Molecule type: mRNA
A;Residues: 1-773 <DEN>
A;Cross-references: GB:X63440; GB:S36169; NID:g416181; PIDN:CAA45037.1; PID:g416182
A;Experimental source: embryonic carcinoma cell, P19 cell
A;Accession: PS0365
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 88-91,'G',93-110,'G',112-118,'S',120,'T',122 <DE2>
A;Experimental source: embryonic carcinoma cell, P19 cell, clone PTP33
A;Accession: PS0369
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 88-91,'G',93-109,'LG',112-120,'T',122 <DE3>
A;Experimental source: embryonic carcinoma cell, P19 cell, clone PTP59
A;Accession: PS0366
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 88-91,'KY',94-109,'LA',112-118,'S',120-122 <DE4>
A;Experimental source: embryonic carcinoma cell, P19 cell, clone PTP42
R;Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A;Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
A;Reference number: A61180; MUID:92032882; PMID:1932742
A;Accession: G61180
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 124-127,'I',129-229 <YIA>
C;Comment: This protein is a located in the cytoplasm.
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosp
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;55-299/Domain: phosphatase catalytic domain #status predicted <PCD>
F;58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
F;231/Active site: Cys (phosphocysteine intermediate) #status predicted
F;237/Binding site: substrate phosphate (Arg) #status predicted

  Query Match           29.3%;  Score 710;  DB 1;  Length 773;
  Best Local Similarity  25.4%;  Pred. No. 5.8e-44;
  Matches  195;  Conservative   88;  Mismatches  162;  Indels  324;  Gaps   20;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|       | :    | :|  ::  |  :: : :  |  | : |||:|||||

Db          8 RRFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:|||||  :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPFRNTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:||||| | |||:|||||    ::|:    | |:   |:    |  :||| : ||
Db        126 VVMIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:   |: |      |:|:|||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMF---------- 292
              ||   ||    ||.:|::|::: :|| || :||||:|||  ::  :||:|
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFENSYNCMKFM 304

Qy        293 ------------------------------------------------------------ 292

Db        305 EHRRSVMVMKLPLELWSVPLIARRDLSAKAAADSKLPCRRGCQGRNTTATRTSPGATHPD 364

Qy        293 -------------CSTLQNAS-------PHYQN--------------------------- 305
                          | |:   :        ||  |
Db        365 AITSFSLPNVTTVCRTVTGTTQSQCCTWPHQSNTQPTSTEAMINQRTNGAKSESAIEHID 424

Qy        306 --IKENCA------PL------YDDALFL-----------------RT--PQALLA---- 328
                :: | :      ||      :|    |                 ||  || | |
Db        425 KKLERNLSPEIKKVPLQEGPKSFDGNTLLNRGHAIKIKSASSSVVDRTSKPQELSAGALK 484

Qy        329 --------------------------------IPRP-------PGGVLRSI-------S 341
                                              |||        | |  |:
Db        485 VDDVSQNSCADCSAAHSHRAAESSEESQSNSHTPPRPDCLPLDKKGHVTWSLHGPENATP 544

Qy        342 VPGSPGHAMADTY--------------AEEQKR---------------------------- 360
              || ||    | :              |||:
Db        545 VPDSPDGKSPDNHSQTLKTVSSTPNSTAEEEAHDLTEHHNSSPLLKAPLSFTNPLHSDDW 604

Qy        361 ----GAPAGAGSGTQTGTGTGA-----RSAEEAPLYSKVTPR--------------AQRP 397
                  |:  || :  :|   | :       |: |:  : :| |                 |::
Db        605 HSDGGSSDGAVTRNKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTPHSGAEKD 664

Qy        398 GAHAEDARGTLPGRVP---------------------------------------------- 413
                :|::   || | |
Db        665 ADVSEESPPPLPERTPESFVLADMPVRPEWHELPNQEWSEQRESEGLTTSGNEKHDAGGI 724

Qy        414 -----ADQSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT 456
                   ||  || |   : :    |:   :||  | |:|||||:|||
Db        725 HTEASADSPPAFSDKKDQITKSPAEVTDIGFGNRCGKPKGPREPPSEWT 773


RESULT 3
JC1368
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN12, nonreceptor type 12 [validated] - huma
N;Alternate names: PTP-PEST; PTPG1
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: JC1368; A47506; A45496; S41746
R;Takekawa, M.; Itoh, F.; Hinoda, Y.; Arimura, Y.; Toyota, M.; Sekiya, M.; Adachi, M.; In
Biochem. Biophys. Res. Commun. 189, 1223-1230, 1992
A;Title: Cloning and characterization of a human cDNA encoding a novel putative cytoplasm
A;Reference number: JC1368; MUID:93112015; PMID:1472029
A;Accession: JC1368
A;Molecule type: mRNA
A;Residues: 1-780 <TAK>
A;Cross-references: UNIPROT:Q05209; DDBJ:D13380; NID:g220033; PIDN:BAA02648.1; PID:g2200
A;Note: the authors translated the codon AGT for residue 636 as Ala
R;Yang, Q.; Co, D.; Sommercorn, J.; Tonks, N.K.
J. Biol. Chem. 268, 17650, 1993
A;Reference number: A47506; MUID:93352561; PMID:8349645
A;Contents: erratum
A;Accession: A47506
A;Molecule type: mRNA
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A;Residues: 1-120,'I',122-321,'I',323-780 <YAN>
A;Cross-references: EMBL:M93425; NID:g292408; PIDN:AAA36529.1; PID:g292409
R;Yang, Q.; Co, D.; Sommercorn, J.; Tonks, N.K.
J. Biol. Chem. 268, 6622-6628, 1993
A;Title: Cloning and expression of PTP-PEST. A novel, human, nontransmembrane protein ty
A;Reference number: A45496; MUID:93203262; PMID:8454633
A;Accession: A45496
A;Molecule type: mRNA
A;Residues: 1-120,'I',122-321,'I',323-494,518-525,'FLLMRKDM' <YA2>
A;Note: sequence extracted from NCBI backbone (NCBIN:127945, NCBIP:127946)
A;Note: sequence has been revised in reference A47506
R;Takekawa, M.; Itoh, F.; Hinoda, Y.; Adachi, M.; Ariyama, T.; Inazawa, J.; Imai, K.; Ya
FEBS Lett. 339, 222-228, 1994
A;Title: Chromosomal localization of the protein tyrosine phosphatase G1 gene and charac
A;Reference number: S41746; MUID:94156037; PMID:7509295
A;Accession: S41746
A;Molecule type: mRNA
A;Residues: 59-127,'YY',130-134,'TE' <TA2>
A;Note: sequence shown is wild type
C;Comment: PEST sequences in this widely expressed protein suggest that it is rapidly de
C;Genetics:
A;Gene: GDB:PTPN12
A;Cross-references: GDB:136846; OMIM:600079
A;Map position: 7q11.23-7q11.23
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosp
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
F;231/Active site: Cys (phosphocysteine intermediate) #status predicted
F;237/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             29.2%;  Score 709;  DB 1;  Length 780;
  Best Local Similarity   41.0%;  Pred. No. 7e-44;
  Matches  144;  Conservative   65;  Mismatches  116;  Indels   26;  Gaps    7;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|        | :   | :|  ::  |  :: : :  |   | : |||:|||||
Db          8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:|||||| :|::||||:|||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMVWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:|||||  | |||:|||||    ::|:    | |:  :::    |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:   |: |     |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :||:|   ||    |
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        303 YQNIKENCAPLYDDALFLRTPQALLAI---------PRPPGGVLRSISVPG 344
                    : |    : |   : :|          |:||    ||  | |
Db        305 ------GAQKIADGVNEINTENMVSSIEPEKQDSPPPKPPR--TRSCLVEG 347


RESULT 4
S48748
protein-tyrosine-phosphatase (EC 3.1.3.48), probable nonreceptor type 12 splice form - r
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S48748
R;Moriyama, T.; Kawanishi, S.; Inoue, T.; Imai, E.; Kaneko, T.; Xia, C.; Takenaka, M.; N
FEBS Lett. 353, 305-308, 1994
A;Title: cDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kidne
A;Reference number: S48748; MUID:95046282; PMID:7957881
A;Accession: S48748
A;Molecule type: mRNA
A;Residues: 1-382 <MOR>
A;Cross-references: UNIPROT:Q63745; GB:D38072; NID:g567262; PIDN:BAA07266.1; PID:g699627
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosph
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
F;231/Active site: Cys (phosphocysteine intermediate) #status predicted
F;237/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             29.1%;  Score 705.5;  DB 1;  Length 382;
  Best Local Similarity   45.1%;  Pred. No. 5.1e-44;
  Matches  133;  Conservative   59;  Mismatches   94;  Indels    9;  Gaps    4;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|        | :   | :|  ::  |  :: : :  |   | : |||:|||||
Db          8 RRFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:|||||| :|::||||:|||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPRAYVATQGPLANTVIDFWRMIWEYN 125

Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
              | :|:|||||  | |||:|||||    ::|:    | |:  |:    |  :||| : ||
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
              ||| :||  |::|||  |||| | :| |:   |: |     |:|:||||||||| :| :
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ 297
              ||   ||    || :|::|::: :|| || :||||:|||  ::  :||:|   ||
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQ 299


RESULT 5
S55345
protein-tyrosine-phosphatase (EC 3.1.3.48) PTP-PEST - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Oct-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S55345; S54261; I48666
R;Charest, A.; Wagner, J.; Shen, S.H.; Tremblay, M.L.
Biochem. J. 308, 425-432, 1995
A;Title: Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyrosine pl
A;Reference number: I48666; MUID:95289971; PMID:7772023
A;Accession: S55345
A;Molecule type: DNA
A;Residues: 1-775 <CHA>
A;Cross-references: UNIPROT:P35831; EMBL:X86781; NID:g804997; PIDN:CAA60477.1; PID:g8049
R;Charest, A.; Wagner, J.; Shen, S.H.; Tremblay, M.L.
submitted to the EMBL Data Library, May 1995
A;Description: Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyro
A;Reference number: S54261
A;Accession: S54261
A;Molecule type: DNA
A;Residues: 1-127,'M',129-309,'R',311-775 <CHW>
A;Cross-references: EMBL:X86781; NID:g804997; PIDN:CAA60477.1; PID:g804998
A;Experimental source: strain BALB/c
C;Genetics:
A;Map position: 5A3-B
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosp
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
F;231/Active site: Cys (phosphocysteine intermediate) #status predicted
F;237/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             29.1%;  Score 705;  DB 2;  Length 775;
  Best Local Similarity   25.0%;  Pred. No. 1.4e-43;
  Matches  194;  Conservative   84;  Mismatches  162;  Indels  336;  Gaps   17;

Qy          9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK 63
              | |::|::|        | :   | :|  ::  |  :: : :  |   | : |||:|||||
Db          8 RRFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65

Qy         64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
              |:||:| :|| |:|      |||||  |||:|| |  ||:|||||| :|::||||::||:
Db         66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPFRNTVIDFWRMIWEYN 125
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Qy        124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
Db        126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFQN 184

Qy        183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
Db        185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ----- 297
Db        245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSAVQTKEQYELVHRAIAQLFEKQLQLYEIH 304

Qy        298 ------------------------------------------------------------ 297
Db        305 GAQKIADGNEITTGTMVSSIDSEKQDSPPPKPPRTRSCLVEGDAKEEILQPPEPHPVPPI 364

Qy        298 ----------------------------NASP--------------------------- 301
Db        365 LTPSPPSAFPTVTTVWQDSDRYHPKPVLHMASPEQHPADLNRSYDKSADQWGKSESAIEH 424

Qy        302 ---------------------------------HYQNIKENCAPLYDDALFLRT--PQA 325
Db        425 IDKKLERNLSFEIKKVPLQEGPKSFDGNTLLNRGHAIKIKSASSSVVD-----RTSKPQE 479

Qy        326 LLA-----------------------------------IPRP-------PGGVLRSI- 340
Db        480 LSAGALKVDDVSQNSCADCSAAHSHRAAESSEESQSNSHTPPRPDCLPLDKKGHVTWSLH 539

Qy        341 ------SVPGSPGHAMADTY--------------AEEQKR---------------------- 360
Db        540 GPENATPVPDSPDGKSPDNHSQTLKTVSSTPNSTAEEEAHDLTEHHNSSPLLKAPLSFTN 599

Qy        361 -----------GAPAGAGSGTQTGTGTGA-----RSAEEAPLYSKVTPR----------- 393
Db        600 PLHSDDWHSDGGSSDGAVTRNKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTP 659

Qy        394 ---AQRPGAHAEDARGTLPGRVP---------------------------------------- 413
Db        660 HSGAEKDADVSEESPPPLPERTPESFVLADMPVRPEWHELPNQEWSEQRESEGLTTSGNE 719

Qy        414 ------------ADQSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT 456
Db        720 KHDAGGIHTEASADSPPAFSDKKDQITKSPAEVTDIGFGNRCGKPKGPREPPSEWT 775
```

RESULT 6
A49724
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
N;Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1; SAP-1
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: A49724
R;Matozaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K
J. Biol. Chem. 269, 2075-2081, 1994
A;Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase an
A;Reference number: A49724; MUID:94124561; PMID:8294459
A;Accession: A49724
A;Molecule type: mRNA
A;Residues: 1-1118 <MATO>
A;Cross-references: UNIPROT:Q15426; GB:D15049; NID:g475003; PIDN:BAA03645.1; PID:g475004
C;Genetics:
A;Gene: GDB:PTPRH; SAP-1
A;Cross-references: GDB:305504
A;Map position: 19q13.4-19q13.4
A;Note: highly expressed in colon and pancreatic cancer cells but not in the normal cell
C;Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III repea
C;Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric monoes
F;1-27/Domain: signal sequence #status predicted <SIG>
F;27-110/Domain: fibronectin type III repeat homology <3FNA>
F;28-1118/Product: protein-tyrosine-phosphatase, receptor type H #status predicted <MAT>
F;28-761/Domain: extracellular #status predicted <EXT>
F;116-199/Domain: fibronectin type III repeat homology <3FNB>
F;205-289/Domain: fibronectin type III repeat homology <3FNC>
F;296-379/Domain: fibronectin type III repeat homology <3FND>
F;385-468/Domain: fibronectin type III repeat homology <3FNE>
F;474-558/Domain: fibronectin type III repeat homology <3FNF>
F;564-658/Domain: fibronectin type III repeat homology <3FNG>
F;667-737/Domain: fibronectin type III repeat homology <3FNH>
F;762-778/Domain: transmembrane #status predicted <TMN>
F;779-1118/Domain: intracellular #status predicted <INT>
F;846-1070/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;35,78,83,107,132,149,172,196,203,286,304,312,329,352,376,383,401,436,439,470,490,558,57
F;1022/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1028/Binding site: substrate phosphate (Arg) #status predicted

  Query Match 20.3%; Score 491.5; DB 1; Length 1118;
  Best Local Similarity 43.3%; Pred. No. 8.4e-28;
  Matches 116; Conservative 36; Mismatches 91; Indels 25; Gaps 9;

```
Qy         47 STVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQG 106
Db        837 SQMVASASENNAKNRYRNVLPYDWSRVPLKPIHEEPGSDYINASFMPGLWSPQEFIATQG 896

Qy        107 PLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITL----I 162
Db        897 PLPQTVGDFWRLVWEQQSHTLVMLTNCMEAGRVKCEHYWPLDSQPCTHGHLRVTLVGEEV 956

Qy        163 KEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARR-----L 217
Db        957 MENWTVRELLL--LQVEEQK-TLSVRQFHYQAWPDHGVPSSPDTLLAFWRMLRQWLDQTM 1013

Qy        218 QGSGPEPLCVHCSAGCGRTGVLCTVD-YVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQ 276
Db       1014 EGGPP---IVHCSAGVGRTGTLIALDVLLRQLQSEGLLGP----FSFVRKMRESRPLMVQ 1066

Qy        277 TEEQYRFLYHTVAQMFCSTLQNASPHYQ 304
Db       1067 TEAQYVFLH----QCICGS-SNSQPRPQ 1089
```

RESULT 7
A44390
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 6 - mouse
N;Alternate names: hematopoietic cell phosphatase (HCP); protein-tyrosine-phosphatase 1C
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 19-May-1994 #text_change 11-Jun-1999
C;Accession: A44390; A42031; F61180; I65741; I52816; I65740; A45143; B45143
R;Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
Mol. Cell. Biol. 12, 2396-2405, 1992
A;Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: c
, and threonine-rich sequences.
A;Reference number: A44390; MUID:92236615; PMID:1373816
A;Accession: A44390
A;Molecule type: mRNA
A;Residues: 1-595 <MAT>
A;Cross-references: GB:M90389; NID:g200550; PIDN:AAA40007.1; PID:g200551
R;Yi, T.L.; Cleveland, J.L.; Ihle, J.N.
Mol. Cell. Biol. 12, 836-846, 1992
A;Title: Protein tyrosine phosphatase containing SH2 domains: characterization, preferent
A;Reference number: A42031; MUID:92123209; PMID:1732748
A;Accession: A42031
A;Molecule type: mRNA
A;Residues: 1-595 <YI1>
A;Cross-references: GB:M68902; NID:g193807
A;Note: sequence extracted from NCBI backbone (NCBIN:76845, NCBIP:76846)
R;Yi, T.; Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
A;Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
A;Reference number: A61180; MUID:92032882; PMID:1932742
A;Accession: F61180
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 342-451 <YIA>
R;Shultz, L.D.; Schweitzer, P.A.; Rajan, T.V.; Yi, T.; Ihle, J.N.; Matthews, R.J.; Thomas
Cell 73, 1445-1454, 1993

A;Title: Mutations at the murine motheaten locus are within the hematopoietic cell prote
A;Reference number: I52816; MUID:93313972; PMID:8324828
A;Accession: I65741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 334-353,359-382 <SHU1>
A;Cross-references: GB:S63803; NID:g388449
A;Note: deletion mutation
A;Accession: I52816
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 350-358,'EGQSPNFLTPTFSSLVLVQYHTQ',359-366 <SHU2>
A;Cross-references: GB:S63763; NID:g388447
A;Note: insertion mutation
A;Accession: I65740
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 34-76,'VPRPHIWRAGGVTAAGQGRALD' <SHU3>
A;Cross-references: GB:S63764; NID:g388450
A;Note: frameshift mutation
R;Yeung, Y.G.; Berg, K.L.; Pixley, F.J.; Angeletti, R.H.; Stanley, E.R.
J. Biol. Chem. 267, 23447-23450, 1992
A;Title: Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine in macrop
A;Reference number: A45143; MUID:93054686; PMID:1385421
A;Accession: A45143
A;Status: preliminary
A;Molecule type: protein
A;Residues: 137-139,'X',141-143,'X',145-151 <YEU>
A;Experimental source: BAC1.2F5 macrophage
A;Note: sequence extracted from NCBI backbone (NCBIP:118519)
A;Accession: B45143
A;Status: preliminary
A;Molecule type: protein
A;Residues: 54-56,'X',58,'X',60-61,'X',63-68 <YE2>
A;Experimental source: BAC1.2F5 macrophage
A;Note: sequence extracted from NCBI backbone (NCBIP:118518)
C;Comment: This protein is found primarily in hematopoietic tissues.
C;Genetics:
A;Gene: me/HCPH; motheaten
C;Function:
A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to release phosphate
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphata
F;4-98/Domain: SH2 homology <SH2A>
F;110-211/Domain: SH2 homology <SH2B>
F;265-521/Domain: phosphatase catalytic domain #status predicted <PHP>
F;270-504/Domain: protein-tyrosine-phosphatase homology <PTP>
F;453/Active site: Cys (phosphocysteine intermediate) #status predicted
F;459/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 475.5; DB 1; Length 595;
Best Local Similarity 36.2%; Pred. No. 5.6e-27;
Matches 106; Conservative 53; Mismatches 105; Indels 29; Gaps 8;

```
Qy         22 EGAVLAG---EFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLL 78
              |    ||   ||  :|      :   :   : | ||||  |||||::||:| :||||
Db        237 EDTAKAGFWEEFESLQ----XQEVKNLHQRLEGQRPENKSKNRYKNILPFDHSRVIL--- 289

Qy         79 QEEGH------SDYINGNFIRGV-----DGSLAYIATQGPLPHTLLDFWRLVWEFGVKVI 127
                :|       ||||| |:::       : |  |||:|| |   |: |||:: |:   :||
Db        290 --QGRDSNIPGSDYINANYVKNQLLGPDENSKTYIASQGCLDATVNDFWQMAWQENTRVI 347

Qy        128 LMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKES--- 184
              :|  ||:| || :|  || :       ||: :|  :|     |   ||||:::
Db        348 VMTTREVEKGRNKCVPYWPEVGTQRVYGLYSVTNSREHDTAE-YKLRTLQISPLDNGDLV 406

Qy        185 RSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPE--PLCVHCSAGCGRTGVLCTV 242
              | ::  ||:|||| |||| |  :|: :::  :| | |    |: ||||| |||| :  :
Db        407 REIWHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVI 466

Qy        243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCST 295
              | : : : |: :  |  :  :  :| ||   |||| ||:|:|  :||   :|
Db        467 DMLMESISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETT 519
```

RESULT 8
A55148
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat
N;Alternate names: OST-PTP; osteotesticular protein-tyrosine-phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55148
R;Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.
J. Biol. Chem. 269, 30659-30667, 1994
A;Title: Identification of a hormonally regulated protein tyrosine phosphatase associatec
A;Reference number: A55148; MUID:95074080; PMID:7527035
A;Accession: A55148
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1711 <MAU>
A;Cross-references: GB:L36884
C;Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosir
C;Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III repe
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prote
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MAT
F;1174-1398/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1350/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 474; DB 1; Length 1711;
Best Local Similarity 39.9%; Pred. No. 2.7e-26;
Matches 114; Conservative 35; Mismatches 111; Indels 26; Gaps 8;

```
Qy         10 SFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYD 69
              || :  ||:           || :::              :    |:|: ||||  |||||
Db       1134 SFRQSYEAKSAHAHQTFFQEFEELKEVGKDQ------PRLEAEHPDNIIKNRYPHVLPYD 1187

Qy         70 QTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILM 129
              :|| |: |  | |||||| ||| |   :   |||||||  || ||||||||  | ||:|
Db       1188 HSRVRLTQLPGEPHSDYINANFIPGYSHTQEIIATQGPLKKTLEDFWRLVWEQQVHVIIM 1247

Qy        130 ACREIENGRKRCERYWAQEQEPLQTGLFCITLIKE----KWLNEDIMLRTLKVTFQKESR 185
              :|||  || ||      |: |   | |: |    :|   :  |:    | ||: |
Db       1248 LTVGMENGRVLCEHYWPANSTPVTHGHITIHLLAEEPEDEWTRREFQLQ--HGTEQKQ-R 1304

Qy        186 SVYQLQYMSWPDRGVPSSPDHMLAMV----EEARRLQGSGPEPLCVHCSAGCGRTGVLCT 241
              | |||: :|||  || :|  :|| |    |: :  || |  |: ||||| ||||
Db       1305 RVKQLQFTTWPDHSVPEAPSSLLAFVELVQEQVQATQGKG--PILVHCSAGVGRTGT--- 1359

Qy        242 VDYVRQLLLTQMIPPD--FSLFDVVLKMRKQRPAAVQTEEQYRFLY 285
              :|  | | : :  :    :|: |  :|  ||  :||  || ||:
Db       1360 --FVALLRLLRQLEEEKVADVFNTVYILRLHRPLMIQTLSQYIFLH 1403
```

RESULT 9
S20825
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN6, nonreceptor type 6 [validated] - human
N;Alternate names: hematopoietic cell phosphatase HCP; protein-tyrosine-phosphatase 1C; P
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: B42031; A38189; S20825; S17234; S20837
R;Yi, T.L.; Cleveland, J.L.; Ihle, J.N.
Mol. Cell. Biol. 12, 836-846, 1992
A;Title: Protein tyrosine phosphatase containing SH2 domains: characterization, preferen
A;Reference number: A42031; MUID:92123209; PMID:1732748
A;Accession: B42031
A;Molecule type: mRNA
A;Residues: 1-595 <YI1>
A;Cross-references: UNIPROT:P29350; GB:M74093
A;Experimental source: T-lymphoid cell line
A;Note: sequence extracted from GenBank
R;Plutzky, J.; Neel, B.G.; Rosenberg, R.D.
Proc. Natl. Acad. Sci. U.S.A. 89, 1123-1127, 1992
A;Title: Isolation of a src homology 2-containing tyrosine phosphatase.
A;Reference number: A38189; MUID:92141214; PMID:1736296

```
A;Accession: A38189
A;Molecule type: mRNA
A;Residues: 1-85,'V',87-595 <PLU>
A;Cross-references: GB:M77273; NID:g338079; PIDN:AAA36610.1; PID:g338080
A;Note: sequence extracted from NCBI backbone (NCBIN:79619, NCBIP:79620)
R;Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.
Nature 353, 868, 1991
A;Title: Corrigendum: A protein-tyrosine phosphatase with sequence similarity to the SH2
A;Reference number: S20825
A;Accession: S20825
A;Molecule type: mRNA
A;Residues: 1,'LSRG',4-595 <SHE>
A;Cross-references: EMBL:X62055; NID:g35781; PIDN:CAA43982.1; PID:g35782
R;Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.
Nature 352, 736-739, 1991
A;Title: A protein-tyrosine phosphatase with sequence similarity to the SH2 domain of th
A;Reference number: S17234; MUID:91343005; PMID:1652101
A;Accession: S17234
A;Molecule type: mRNA
A;Residues: 1,'LSRG',4-589,'VPSRGSERCCPQVAMPQP' <SH2>
A;Experimental source: breast carcinoma cells
A;Note: sequence revised in reference S20805
C;Genetics:
A;Gene: GDB:PTPN6
A;Cross-references: GDB:131389; OMIM:176883
A;Map position: 12p13-12p13
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;4-98/Domain: SH2 homology <SH2A>
F;110-211/Domain: SH2 homology <SH2B>
F;265-521/Domain: phosphatase catalytic domain #status predicted <PHP>
F;270-504/Domain: protein-tyrosine-phosphatase homology <PTP>
F;453/Active site: Cys (phosphocysteine intermediate) #status predicted
F;459/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             19.1%;  Score 463;  DB 1;  Length 595;
  Best Local Similarity   32.9%;  Pred. No. 4.6e-26;
  Matches  112;  Conservative   56;  Mismatches  110;  Indels   62;  Gaps   10;

Qy          22 EGAVLAG---EFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLL 78
               |    ||    ||  :|       :   :   : | ||||  |||||::||:| :||||
Db         237 EDTAKAGFWEEFESLQ----KQEVKNLHQRLEGQRPENKGKNRYKNILPFDHSRVIL--- 289

Qy          79 QEEGH------SDYINGNFIRGV-----DGSLAYIATQGPLPHTLLDFWRLVWEFGVKVI 127
                 :|       ||||| |:|:       : :  |||:|| |   |: |||:: |:   :||
Db         290 --QGRDSNIPGSDYINANYIKNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVI 347

Qy         128 LMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKES--- 184
               :|  ||:| || :|  ||  :       | : :|    |     |   ||||:|:
Db         348 VMTTREVEKGRNKCVPYWPEVGMQRAYGPYSVTNCGEHDTTE-YKLRTLQVSPLDNGDLI 406

Qy         185 RSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPE--PLCVHCSAGCGRTGVLCTV 242
               | ::  ||:|||| |||| |  :|: :::  : | | |   |: |||||| |||| :  :
Db         407 REIWHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVI 466

Qy         243 DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCST------- 295
               | : : : |: :  |  :   :  :| ||   |||| ||:|:|  :||   :|
Db         467 DMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVL 526

Qy         296 ------------------LQNA--------SPHYQNIKEN 309
                               ::||         | | ::: ||
Db         527 QSQKGQESEYGNITYPPAMKNAHAKASRTSSKHKEDVYEN 566


RESULT 10
A41105
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human
N;Alternate names: PTPase MEG
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C;Accession: A41105
R;Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
A;Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty
A;Reference number: A41105; MUID:91288564; PMID:1648233
A;Accession: A41105
A;Molecule type: mRNA
A;Residues: 1-926 <GUA>
A;Cross-references: UNIPROT:P29074; GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748
A;Experimental source: megakaryocytes, cell line MEG-10
C;Genetics:
A;Gene: GDB:PTPN4
A;Cross-references: GDB:131387; OMIM:176878
A;Map position: 9q31-9q31
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; p
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F;523-597/Domain: GLGF domain homology <GLG>
F;679-900/Domain: protein-tyrosine-phosphatase homology <PTP>
F;852/Active site: Cys (phosphocysteine intermediate) #status predicted
F;858/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             19.1%;  Score 462;  DB 1;  Length 926;
  Best Local Similarity   37.6%;  Pred. No. 9.4e-26;
  Matches  106;  Conservative   47;  Mismatches  107;  Indels   22;  Gaps    9;

Qy          17 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 76
               |  |   | ||  :|  :       |  |:  : |   |:|: ||||:|: ||| |||||
Db         647 AEGLITGTVLT-QFDQLYR-----KKPGMTMSCA-KLPQNISKNRYRDISPYDATRVIL- 698

Qy          77 LLQEEGHSDYINGNFIRGVDGSLA----YIATQGPLPHTLLDFWRLVWEFGVKVILMACR 132
                   :|: |||| |:|      | :    ||| |||||||  |||:: || |  :::|
Db         699 ----KGNEDYINANYINMEIPSSSIINQYIACQGPLPHTCTDFWQMTWEQGSSMVVMLTT 754

Qy         133 EIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK--ESRSVYQL 190
               ::| || :| :|| :       | : :|    |:  |   : | : :  |:  ||| : |:
Db         755 QVERGRVKCHQYWPEPTGSSSYGCYQVTCHSEEG-NTAYIFRKMTLFNQEKNESRPLTQI 813

Qy         191 QYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLL 250
               ||:|||| |||      |  |   :    ||: |||||| |||||| |::      : |
Db         814 QYIAWPDHGVPDDSSDFLDFVCHVRNKRAGKEEPVVVHCSAGIGRTGVLITME--TAMCL 871

Qy         251 TQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMF 292
                 :   | : | |:|  || ||   :||  ||||:   : :::
Db         872 IECNQPVYPL-DIVRTMRDQRAMMIQTPSQYRFVCEAILKVY 912


RESULT 11
JN0805
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN11, nonreceptor type 11 [validated] - huma
N;Alternate names: BPTP-3; protein-tyrosine-phosphatase SHP-2; PTP1D; PTP2C; SH-PTP2; SH-
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: JN0805; A46210; A47386; A47244; S27398; C44929; S31767
R;Bastien, L.; Ramachandran, C.; Liu, S.; Adam, M.
Biochem. Biophys. Res. Commun. 196, 124-133, 1993
A;Title: Cloning, expression and mutational analysis of SH-PTP2, human protein-tyrosine p
A;Reference number: JN0805; MUID:94029983; PMID:8216283
A;Accession: JN0805
A;Molecule type: mRNA
A;Residues: 1-593 <BAS>
A;Cross-references: UNIPROT:Q06124; GB:L07527; NID:g292406; PIDN:AAA17022.1; PID:g292407
R;Vogel, W.; Lammers, R.; Huang, J.; Ullrich, A.
Science 259, 1611-1614, 1993
A;Title: Activation of a phosphotyrosine phosphatase by tyrosine phosphorylation.
A;Reference number: A46210; MUID:93206095; PMID:7681217
A;Accession: A46210
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-593 <VOG>
A;Cross-references: EMBL:X70766; NID:g35783; PIDN:CAA50045.1; PID:g35784
A;Experimental source: SK-BR-3 mammary carcinoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:127775)
R;Ahmad, S.; Banville, D.; Zhao, Z.; Fischer, E.H.; Shen, S.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 2197-2201, 1993
A;Title: A widely expressed human protein-tyrosine phosphatase containing src homology 2
```

A;Reference number: A47386; MUID:93211929; PMID:7681589
A;Accession: A47386
A;Molecule type: mRNA
A;Residues: 1-593 <AHM>
A;Experimental source: umbilical cord
A;Note: sequence extracted from NCBI backbone (NCBIN:128129, NCBIP:128131)
R;Freeman Jr., R.M.; Plutzky, J.; Neel, B.G.
Proc. Natl. Acad. Sci. U.S.A. 89, 11239-11243, 1992
A;Title: Identification of a human src homology 2-containing protein-tyrosine-phosphatas
A;Reference number: A47244; MUID:93087502; PMID:1280823
A;Accession: A47244
A;Molecule type: mRNA
A;Residues: 1-593 <FRE>
A;Cross-references: GB:L03535; NID:g338081; PIDN:AAA36611.1; PID:g338082
A;Note: sequence extracted from NCBI backbone (NCBIN:119760, NCBIP:119761)
R;Adachi, M.; Sekiya, M.; Miyachi, T.; Matsuno, K.; Hinoda, Y.; Imai, K.; Yachi, A.
FEBS Lett. 314, 335-339, 1992
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase SH-PTP3 with sequence
A;Reference number: S27398; MUID:93106179; PMID:1281790
A;Accession: S27398
A;Molecule type: mRNA
A;Residues: 1-534,'R',536-547,'P',549-593 <AD2>
A;Cross-references: DDBJ:D13540; NID:g220071; PIDN:BAA02740.2; PID:g4519425
R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yac
Cancer Res. 52, 737-740, 1992
A;Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A;Reference number: A44929; MUID:92119637; PMID:1370651
A;Accession: C44929
A;Molecule type: mRNA
A;Residues: 'Q',370-460 <ADA>
A;Cross-references: GB:S78088; NID:g243547; PIDN:AAB21148.1; PID:g243548
A;Experimental source: pre-B cell NALM-6
A;Note: sequence extracted from NCBI backbone (NCBIN:78088, NCBIP:78089)
A;Note: the authors did not report the entire codon for residue 92
C;Comment: This ubiquitous enzyme plays a critical role in regulating physiological cell
C;Genetics:
A;Gene: GDB:PTPN11
A;Cross-references: GDB:137093; OMIM:176876
A;Map position: 12q24.1-12q24.1
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;6-100/Domain: SH2 homology <SH2A>
F;112-214/Domain: SH2 homology <SH2B>
F;273-510/Domain: protein-tyrosine-phosphatase homology <PTP>
F;459/Active site: Cys (phosphocysteine intermediate) #status predicted
F;465/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.7%; Score 453; DB 1; Length 593;
Best Local Similarity 33.8%; Pred. No. 2.4e-25;
Matches 119; Conservative 53; Mismatches 126; Indels 54; Gaps 12;

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Qy          1 MSRSLDSARSFLERLEARGGREGAVLA-----------GEFSDI--QACSAAWKADGVCS 47
              : : |:: |      :|:|  || : ||             ||  :  | |   :      |
Db        212 LKQPLNTTRINAAEIESR-VRELSKLAETTDKVKQGFWEEFETLQQQECKLLY------S 264

Qy         48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGH-----SDYINGNFI--------RG 94
                | | ||  |||||::||:| |||:|      :|      |||| | |
Db        265 RKEGQRQENKNKNRYKNILPFDHTRVVL----HDGDPNEPVSDYINANIIMPEFETKCNN 320

Qy         95 VDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQT 154
                :||||| | :|: ||||:|::   :||:|  :|:| |: :| :||  |    :
Db        321 SKPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWPDEYALKEY 380

Qy        155 GLFCITLIKEKWLNEDIMLRTLKVTFQKE---SRSVYQLQYMSWPDRGVPSSPDHMLAMV 211
              |:  :  :||      |  || ||::   :    |:|:|  : :||| |||| |  :|  :
Db        381 GVMRVRNVKES-AAHDYTLRELKLSKVGQGNTERTVWQYHFRTWPDHGVPSDPGGVLDFL 439

Qy        212 EEARRLQGS--GPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVLKMRK 269
              ||    | |      |: ||||| ||||    :| :  ::  : :  |  :   :  :|
Db        440 EEVHHKQESIMDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRS 499

Qy        270 QRPAAVQTEEQYRFLYHTVAQMFCSTLQ----------NASPHYQNIKENCA 311
              ||   |||| ||||:|  | | :  |||              | ||| : |
Db        500 QRSGMVQTEAQYRFIYMAV-QHYIETLQRRIEEEQKSKRKGHEYTNIKYSLA 550
```

RESULT 12
JC5167
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - chicken
N;Alternate names: phosphotyrosine phosphatase; PTP1D; PTP2c; SH-PTP2; SyP
C;Species: Gallus gallus (chicken)
C;Date: 21-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: JC5167
R;Park, C.Y.; LaMontagne, K.R.; Tonks, N.K.; Hayman, M.J.
Gene 177, 93-97, 1996
A;Title: Cloning and expression of the chicken protein tyrosine phosphatase SH-PTP2.
A;Reference number: JC5167; MUID:97080506; PMID:8921851
A;Contents: erythroblast
A;Accession: JC5167
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-593 <PAR>
A;Cross-references: UNIPROT:Q90687; GB:U38620; NID:g1054939; PIDN:AAC60049.1; PID:g105494
C;Comment: This enzyme plays positive roles in mitogenic signaling and early development.
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phospha
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;6-105,112-193/Domain: SH2 #status predicted <SH2>
F;6-100/Domain: SH2 homology <SH2A>
F;112-214/Domain: SH2 homology <SH2B>
F;273-510/Domain: protein-tyrosine-phosphatase homology <PTP>
F;559-570/Region: proline-rich
F;459/Active site: Cys (phosphocysteine intermediate) #status predicted
F;465/Binding site: substrate phosphate (Arg) #status predicted
F;542,547,580/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 18.7%; Score 453; DB 2; Length 593;
Best Local Similarity 33.9%; Pred. No. 2.4e-25;
Matches 118; Conservative 53; Mismatches 123; Indels 54; Gaps 12;

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Qy          1 MSRSLDSARSFLERLEARGGREGAVLA-----------GEFSDI--QACSAAWKADGVCS 47
              : : |:: |      :|:|  || : ||             ||  :  | |   :      |
Db        212 LKQPLNTTRINAAEIESR-VRELSKLAETTDKVKQGFWEEFETLQQQECKLLY------S 264

Qy         48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGH-----SDYINGNFI--------RG 94
                | | ||  |||||::||:| |||:|      :|      |||| | |
Db        265 RKEGQRQENKNKNRYKNILPFDHTRVVL----HDGDPNEPVSDYINANIIMPEFETKCNN 320

Qy         95 VDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQT 154
                :||||| | :|: ||||:|::   :||:|  :|:| |: :| :||  |    :
Db        321 SKPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWPDEYSLKEY 380

Qy        155 GLFCITLIKEKWLNEDIMLRTLKVTFQKE---SRSVYQLQYMSWPDRGVPSSPDHMLAMV 211
              |:  :  :||      |  || ||::   :    |:|:|  : :||| |||| |  :|  :
Db        381 GVMRVRNVKES-AAHDYTLRELKLSKVGQGNTERTVWQYHFRTWPDHGVPSDPGGVLDFL 439

Qy        212 EEARRLQGSGPE--PLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVLKMRK 269
              ||    | |  :  |: |||||| ||||    :| :  ::  : :  |  :   :  :|
Db        440 EEVHHKQESISDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRS 499

Qy        270 QRPAAVQTEEQYRFLYHTVAQMFCSTLQ----------NASPHYQNIK 307
              ||   |||| ||||:|  | | :  |||              | |||
Db        500 QRSGMVQTEAQYRFIYMAV-QHYIETLQRRIEEEQKSKRKGHEYTNIK 546
```

RESULT 13
A46209
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - mouse
N;Alternate names: SH-PTP2; SH2-containing phosphotyrosine phosphatase Syp
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46209
R;Feng, G.S.; Hui, C.C.; Pawson, T.
Science 259, 1607-1611, 1993
A;Title: SH2-containing phosphotyrosine phosphatase as a target of protein-tyrosine kina
A;Reference number: A46209; MUID:93206094; PMID:8096088
A;Accession: A46209

```
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-585 <FEN>
A;Cross-references: UNIPROT:P35235
A;Note: sequence extracted from NCBI backbone (NCBIP:127770)
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;6-100/Domain: SH2 homology <SH2A>
F;112-214/Domain: SH2 homology <SH2B>
F;273-514/Domain: protein-tyrosine-phosphatase homology <PTP>
F;463/Active site: Cys (phosphocysteine intermediate) #status predicted
F;469/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             18.6%;  Score 451;  DB 2;  Length 585;
  Best Local Similarity   31.0%;  Pred. No. 3.4e-25;
  Matches  128;  Conservative   59;  Mismatches  142;  Indels   84;  Gaps   15;

Qy          1 MSRSLDSARSFLERLEARGGREGAVLA----------GEFSDI--QACSAAWKADGVCS 47
              : : |:: |     :|:|  || : ||           ||  :  | |   :      |
Db        212 LKQPLNTTRINAAEIESR-VRELSKLAETTDKVKQGFWEEFETLQQQECKLLY------S 264

Qy         48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGH-----SDYINGNFI--------RG 94
                | | ||  |||||::||:| |||:|     :|      |||||  | |
Db        265 RKEGQRQENKNKNRYKNILPFDHTRVVL----HDGDPNEPVSDYINANIIMPEFETKCNN 320

Qy         95 VDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQT 154
                :||||||  | :|: ||||:|::   :||:|  :|:| |: :| :||  |    :
Db        321 SKPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWPDEYALKEY 380

Qy        155 GLFCITLIKEKWLNEDIMLRTLKVTFQKES-------RSVYQLQYMSWPDRGVPSSPDHM 207
              |:  :  :||     |  || ||:: .  ::       |:|:|  : :||| |||| |  :
Db        381 GVMRVRNVKES-AAHDYTLRELKLSKVGQALLQGNTERTVWQYHFRTWPDHGVPSDPGGV 439

Qy        208 LAMVEEARRLQGS--GPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
              |  :||    | |     |: ||||||  ||||    :| :  ::  : :  |  :   :
Db        440 LDFLEEVHHKQESIVDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQ 499

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ----------NASPHYQNIKENCAPLYD 315
              :| ||   |||| ||||:|  | | :  |||               |  |||      |
Db        500 MVRSQRSGMVQTEAQYRFIYMAV-QHYIETLQRRIEEEQKSKRKGHEYTNIK------YS 552

Qy        316 DALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKRGAPAGAGS 368
                |    :                 | |||:::    :|   |    | |:
Db        553 GELGYTETRV-----------------GCPGHSVSP--MDEVDGGWVEGLGT 585


RESULT 14
A53593
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - rat
N;Alternate names: PTPase L1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A53593; S29281
R;Mei, L.; Doherty, C.A.; Huganir, R.L.
J. Biol. Chem. 269, 12254-12262, 1994
A;Title: RNA splicing regulates the activity of a SH2 domain-containing protein tyrosine
A;Reference number: A53593; MUID:94216346; PMID:7512964
A;Accession: A53593
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-597 <MEI>
A;Cross-references: UNIPROT:P41499; GB:U05963; NID:g458332; PIDN:AAA19133.1; PID:g458333
R;Hiraga, A.; Munakata, H.; Hata, K.; Suzuki, Y.; Tsuiki, S.
Eur. J. Biochem. 209, 195-206, 1992
A;Title: Purification and characterization of a rat liver protein-tyrosine phosphatase w
A;Reference number: S29281; MUID:93011127; PMID:1382983
A;Accession: S29281
A;Molecule type: protein
A;Residues: 24-31;36-54;56-89;100-103,'X',105-108;'X',113-120;132-155;179-198;214-233;24
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
F;6-100/Domain: SH2 homology <SH2A>
F;112-214/Domain: SH2 homology <SH2B>
F;273-514/Domain: protein-tyrosine-phosphatase homology <PTP>
F;463/Active site: Cys (phosphocysteine intermediate) #status predicted
F;469/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             18.5%;  Score 449;  DB 1;  Length 597;
  Best Local Similarity   32.4%;  Pred. No. 4.8e-25;
  Matches  125;  Conservative   58;  Mismatches  141;  Indels   62;  Gaps   14;

Qy          1 MSRSLDSARSFLERLEARGGREGAVLA----------GEFSDI--QACSAAWKADGVCS 47
              : : |:: |     :|:|  || : ||           ||  :  | |   :      |
Db        212 LKQPLNTTRINAAEIESR-VRELSKLAETTDKVKQGFWEEFETLQQQECKLLY------S 264

Qy         48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGH-----SDYINGNFI--------RG 94
                | | ||  |||||::||:| |||:|     :|      |||||  | |
Db        265 RKEGQRQENKNKNRYKNILPFDHTRVVL----HDGDPNEPVSDYINANIIMPEFETKCNN 320

Qy         95 VDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQT 154
                :||||||  | :|: ||||:|::   :||:|  :|:| |: :| :||  |    :
Db        321 SKPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWPDECALKEY 380

Qy        155 GLFCITLIKEKWLNEDIMLRTLKVTFQKES-------RSVYQLQYMSWPDRGVPSSPDHM 207
              |:  :  ::|     |  || ||::   ::       |:|:|  : :||| |||| |  :
Db        381 GVMRVRNVRES-AAHDYTLRELKLSKVGQALLQGNTERTVWQYHFRTWPDHGVPSDPGGV 439

Qy        208 LAMVEEARRLQGS--GPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
              |  :||    | |     |: ||||||  ||||    :| :  ::  : :  |  :   :
Db        440 LDFLEEVHHKQESIVDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQ 499

Qy        266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ----------NASPHYQNIKENCAPLYD 315
              :| ||   |||| ||||:|  | | :  |||               |  |||      |
Db        500 MVRSQRSGMVQTEAQYRFIYMAV-QHYIETLQRRIEEEQKSKRKGHEYTNIKSS---LVD 555

Qy        316 DALFLRTPQALLAIPRPPGGVLRSIS 341
                ::|     | ||   :|  |
Db        556 QTSGDQSPLP-PCTPTPPCAEMREDS 580


RESULT 15
A44267
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - slime mold (Dictyostelii
C;Species: Dictyostelium discoideum
C;Date: 30-Apr-1993 #sequence_revision 08-Mar-1996 #text_change 24-Apr-1998
C;Accession: A44267
R;Howard, P.K.; Sefton, B.M.; Firtel, R.A.
Cell 71, 637-647, 1992
A;Title: Analysis of a spatially regulated phosphotyrosine phosphatase identifies tyrosir
A;Reference number: A44267; MUID:93046662; PMID:1423620
A;Accession: A44267
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA; DNA
A;Residues: 1-521 <HOW>
A;Note: sequence extracted from NCBI backbone (NCBIP:117713)
C;Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 1; protein-ty
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;121-459/Domain: protein-tyrosine-phosphatase homology #status atypical <PTP>
F;310/Active site: Cys (phosphocysteine intermediate) #status predicted
F;316/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             18.5%;  Score 448;  DB 1;  Length 521;
  Best Local Similarity   29.0%;  Pred. No. 4.8e-25;
  Matches  113;  Conservative   53;  Mismatches   88;  Indels  136;  Gaps   13;

Qy         44 GVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSL--AY 101
              |   | | :  |  |||| ::|| : ||| |  :|::  ||||| |:|   ||:    :
Db        109 GPSETSEGDKKHNTSKNRYTNILPVNHTRVQLKKIQDKEGSDYINANYI---DGAYPKQF 165

Qy        102 IATQGPLPHTLLDFWRLVWEPGVKVILMACREIENGRKRCERYWAQEQEPLQTGLF---- 157
              | ||||||:|: ||||:|||   ::|:|  || || | :|:||| ::     |  ::
Db        166 ICTQGPLPNTIADFWRMVWENRCRIIVMLSRESENCRIKCDRYWPEQIGGEQFSIYGNGN 225

Qy        158 ---------CITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPDH-- 206
                      : :|::     :|: | :::||: |:| : | ||  |||  :   |||
Db        226 EVFGTYSVELVEVIQDP--EREIITRNIRLTFEGETRDITQYQYEGWPDHNI---PDHTQ 280
```

```
Qy        207 -----MLAMVEEARRLQGSGPE--PLCVHCSAGCGRTGVLCTV--------DYVRQLLLT 251
              : ::     ::  |     |: |||||| |||| ||          | :|| |
Db        281 PFRQLLHSITNRQNQIIPSSDRNVPIIVHCSAGVGRTGTFCTAVIMMKKLDHYFKQLDAT 340

Qy        252 ---QMIPP---------------------------------------------------- 256
                |:: |
Db        341 PIDQVVDPFTHLPITEYQSDNLDLKGLGYHFKSSIYNSNGINNNNNNNLNNNNNINNNSN 400

Qy        257 ----------------------------------DFSLFDVVLKMRKQRPAAVQTEEQY 281
                                                ||:|| :|||:|:|||  ||  |||
Db        401 GSNNTPQTEPNNEEDDDDAAESTKYAIMDKYNSRIDFNLFSIVLKLREQRPGMVQQLEQY 460

Qy        282 RFLYHTV-AQMF----CSTLQNASPHYQNI 306
               | | |: |:::    |  |  : ||  ||
Db        461 LFCYKTILAEIYHRLNCK-LGFSLPHVNNI 489
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Search completed: December 7, 2004, 09:50:20
Job time : 43 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:54:33 ; Search time 21 Seconds
(without alignments)
1446.364 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 458
Sequence: 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size: 12

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	155	33.8	155	3	US-08-821-278A-17	Sequence 17, Appl
2	32	7.0	453	3	US-08-821-278A-2	Sequence 2, Appli
3	29	6.3	453	3	US-08-951-260A-7	Sequence 7, Appli
4	29	6.3	453	4	US-09-430-626A-7	Sequence 7, Appli
5	29	6.3	453	4	US-10-243-687-7	Sequence 7, Appli
6	20	4.4	20	3	US-08-938-830-20	Sequence 20, Appl
7	20	4.4	20	3	US-09-020-222-20	Sequence 20, Appl
8	12	2.6	541	4	US-09-248-796A-18318	Sequence 18318, A

ALIGNMENTS

RESULT 1
US-08-821-278A-17
; Sequence 17, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 17
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-17

Query Match 33.8%; Score 155; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.2e-134;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 60

Qy         77 LLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIEN 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIEN 120

Qy        137 GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 171
              |||||||||||||||||||||||||||||||||||
Db        121 GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 155
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RESULT 2
US-08-821-278A-2
; Sequence 2, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Mus Musculus
US-08-821-278A-2

Query Match 7.0%; Score 32; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 5.1e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        100 AYIATQGPLPHTLLDFWRLVWEFGVKVILMAC 131
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RESULT 3
US-08-951-260A-7
; Sequence 7, Application US/08951260A
; Patent No. 6004791
; GENERAL INFORMATION:
; APPLICANT: Aoki, Naohito
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
; TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:

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;       APPLICATION NUMBER:  US/08/951,260A
;       FILING DATE:  October 16, 1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/030,860
;       FILING DATE:  No. 6004791ember 13, 1996
;       APPLICATION NUMBER:  PCT/1897/00946
;       FILING DATE:  June 17, 1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  227/004
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  453 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-951-260A-7

  Query Match             6.3%;  Score 29;  DB 3;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-18;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        430 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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Db        425 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453


RESULT 4
US-09-430-626A-7
; Sequence 7, Application US/09430626A
; Patent No. 6482605
;   GENERAL INFORMATION:
;       APPLICANT: Aoki, Naohito
;                  Ullrich, Axel
;       TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
;                           AND RELATED PRODUCTS AND METHODS
;       NUMBER OF SEQUENCES: 7
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lyon & Lyon
;            STREET: 633 West Fifth Street
;                    Suite 4700
;            CITY: Los Angeles
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 90071-2066
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                         storage
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: IBM P.C. DOS 5.0
;            SOFTWARE: FastSEQ for Windows 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/430,626A
;            FILING DATE: 29-Oct-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/951,260
;            FILING DATE: October 16, 1997
;            APPLICATION NUMBER: 60/030,860
;            FILING DATE: No. 6482605ember 13, 1996
;            APPLICATION NUMBER: PCT/1897/00946
;            FILING DATE: June 17, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Warburg, Richard J.
;            REGISTRATION NUMBER: 32,327
;            REFERENCE/DOCKET NUMBER: 227/004
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (213) 489-1600
;            TELEFAX: (213) 955-0440
;            TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 453 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-430-626A-7

  Query Match             6.3%;  Score 29;  DB 4;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-18;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        430 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |||||||||||||||||||||||||||||
Db        425 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453


RESULT 5
US-10-243-687-7
; Sequence 7, Application US/10243687
; Patent No. 6797501
;   GENERAL INFORMATION:
;       APPLICANT: Aoki, Naohito
;                  Ullrich, Axel
;       TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
;                           AND RELATED PRODUCTS AND METHODS
;       NUMBER OF SEQUENCES: 7
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lyon & Lyon
;            STREET: 633 West Fifth Street
;                    Suite 4700
;            CITY: Los Angeles
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 90071-2066
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                         storage
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: IBM P.C. DOS 5.0
;            SOFTWARE: FastSEQ for Windows 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/243,687
;            FILING DATE: 16-Sep-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/430,626A
;            FILING DATE: 29-Oct-1999
;            APPLICATION NUMBER: 08/951,260
;            FILING DATE: October 16, 1997
;            APPLICATION NUMBER: 60/030,860
;            FILING DATE: No. 6797501ember 13, 1996
;            APPLICATION NUMBER: PCT/1897/00946
;            FILING DATE: June 17, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Warburg, Richard J.
;            REGISTRATION NUMBER: 32,327
;            REFERENCE/DOCKET NUMBER: 227/004
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (213) 489-1600
;            TELEFAX: (213) 955-0440
;            TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 453 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-243-687-7

Query Match 6.3%; Score 29; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 430 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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Db 425 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453

RESULT 6
US-08-938-830-20
; Sequence 20, Application US/08938830
; Patent No. 6040437
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; APPLICANT: Dowbenko, Donald J.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPs)
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,830
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-938-830-20

Query Match 4.4%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 GFNLRIGRPKGPRDPPAEWT 456
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Db 1 GFNLRIGRPKGPRDPPAEWT 20

RESULT 7
US-09-020-222-20
; Sequence 20, Application US/09020222
; Patent No. 6111073
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPS)
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,222
; FILING DATE: 06-Feb-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 02/07/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-020-222-20

Query Match 4.4%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 GFNLRIGRPKGPRDPPAEWT 456
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Db 1 GFNLRIGRPKGPRDPPAEWT 20

RESULT 8
US-09-248-796A-18318
; Sequence 18318, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18318
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18318

Query Match 2.6%; Score 12; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 443 VHCSAGCGRTGV 454

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Job time : 21 secs

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:55:38 ; Search time 147 Seconds
(without alignments)
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Title: US-10-087-993A-36
Perfect score: 458
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1582225 seqs, 356638895 residues

Word size : 12

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	458	100.0	458	13	US-10-087-993-36	Sequence 36, Appl
2	29	6.3	453	14	US-10-243-687-7	Sequence 7, Appli
3	24	5.2	448	13	US-10-087-993-32	Sequence 32, Appl
4	20	4.4	20	14	US-10-340-288-13	Sequence 13, Appl
5	12	2.6	750	9	US-09-801-368-280	Sequence 280, App
6	12	2.6	750	14	US-10-369-493-22392	Sequence 22392, A

ALIGNMENTS

RESULT 1
US-10-087-993-36

; Sequence 36, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Naylor, Oliver
; Kharitonenkov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
; AND SIRP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303Alember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303Alember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-087-993-36

Query Match 100.0%; Score 458; DB 13; Length 458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
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Db         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
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Db        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300

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Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420
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Qy        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |||||||||||||||||||||||||||||||||||||
Db        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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RESULT 2
US-10-243-687-7
; Sequence 7, Application US/10243687
; Publication No. US20030073120A1
;   GENERAL INFORMATION:
;        APPLICANT: Aoki, Naohito
;                   Ullrich, Axel
;        TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
;                            AND RELATED PRODUCTS AND METHODS
;        NUMBER OF SEQUENCES: 7
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/243,687
;             FILING DATE: 16-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/430,626A
;             FILING DATE: 29-Oct-1999
;             APPLICATION NUMBER: 08/951,260
;             FILING DATE: October 16, 1997
;             APPLICATION NUMBER: 60/030,860
;             FILING DATE: No. US20030073120A1ember 13, 1996
;             APPLICATION NUMBER: PCT/1897/00946
;             FILING DATE: June 17, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 227/004
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 453 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-243-687-7

  Query Match             6.3%;  Score 29;  DB 14;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-18;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        430 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |||||||||||||||||||||||||||||
Db        425 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453
```

```
RESULT 3
US-10-087-993-32
; Sequence 32, Application US/10087993
; Publication No. US20020169303A1
;   GENERAL INFORMATION:
;        APPLICANT: Ullrich, Axel
;                   Aoki, Nachito
;                   Kim, Yeong Woong
;                   Wang, Hong Yang
;                   Chen, Zhengjun
;                   Naylor, Oliver
;                   Kharitonenkov, Alexei Igorevich
;        TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
;                            AND SIRP POLYPEPTIDES AND RELATED
;                            PRODUCTS AND METHODS
;        NUMBER OF SEQUENCES: 38
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/087,993
;             FILING DATE: 05-Mar-2002
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/877,150
;             FILING DATE: June 17, 1997
;             APPLICATION NUMBER: U.S. 60/019,629
;             FILING DATE: June 17, 1996
;             APPLICATION NUMBER: U.S. 60/023,485
;             FILING DATE: August 9, 1996
;             APPLICATION NUMBER: U.S. 60/030,860
;             FILING DATE: No. US20020169303A1ember 13, 1996
;             APPLICATION NUMBER: U.S. 60/034,286
;             FILING DATE: December 19, 1996
;             APPLICATION NUMBER: U.S. 60/030,964
;             FILING DATE: No. US20020169303A1ember 15, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 225/298
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
```

; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-087-993-32

Query Match 5.2%; Score 24; DB 13; Length 448;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 AYIATQGPLPHTLLDFWRLVWEFG 123
||||||||||||||||||||||||
Db 100 AYIATQGPLPHTLLDFWRLVWEFG 123

RESULT 4
US-10-340-288-13
; Sequence 13, Application US/10340288
; Publication No. US20030170855A1
; GENERAL INFORMATION:
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University
; APPLICANT: ZHANG, Zhong-Yin
; APPLICANT: XIE, Laiping
; APPLICANT: ZHANG, Yan-Ling
; TITLE OF INVENTION: A NOVEL PROTEIN TYROSINE PHOSPHATASE SUBSTRATE-TRAPPING DOUBLE
; TITLE OF INVENTION: MUTANT AND USES THEREOF
; FILE REFERENCE: 96700/792
; CURRENT APPLICATION NUMBER: US/10/340,288
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/347,413
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-288-13

Query Match 4.4%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 VVLKMRKQRPAAVQTEEQYR 282
||||||||||||||||||||
Db 1 VVLKMRKQRPAAVQTEEQYR 20

RESULT 5
US-09-801-368-280
; Sequence 280, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-280

Query Match 2.6%; Score 12; DB 9; Length 750;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCSAGCGRTGV 238
||||||||||||
Db 664 VHCSAGCGRTGV 675

RESULT 6
US-10-369-493-22392
; Sequence 22392, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22392
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22392

Query Match 2.6%; Score 12; DB 14; Length 750;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCSAGCGRTGV 238
||||||||||||
Db 664 VHCSAGCGRTGV 675

Search completed: December 7, 2004, 10:02:57
Job time : 147 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:53:48 ; Search time 19 Seconds
(without alignments)
2319.330 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 458
Sequence: 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 12

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	2.6	750	2	S67100	protein-tyrosine-p

ALIGNMENTS

RESULT 1
S67100
protein-tyrosine-phosphatase (EC 3.1.3.48) PTP2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O4849; protein YOR208w
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67100; A42667; A41980; S31554; S14170; JC1484; S42155
R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S67100
A;Molecule type: DNA
A;Residues: 1-750 <HUG>
A;Cross-references: UNIPROT:P29461; EMBL:Z75116; NID:g1420486; PID:e252394; PID:g1420487
A;Experimental source: strain S288C
R;Guan, K.L.; Deschenes, R.J.; Dixon, J.E.
J. Biol. Chem. 267, 10024-10030, 1992
A;Title: Isolation and characterization of a second protein tyrosine phosphatase gene, P
A;Reference number: A42667; MUID:92250559; PMID:1577774
A;Accession: A42667
A;Molecule type: DNA
A;Residues: 1-473,'NV',476-750 <GUA>
A;Cross-references: GB:M85287
R;Ota, I.M.; Varshavsky, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2355-2359, 1992
A;Title: A gene encoding a putative tyrosine phosphatase suppresses lethality of an N-enc
A;Reference number: A41980; MUID:92196117; PMID:1549598
A;Accession: A41980
A;Molecule type: DNA
A;Residues: 1-750 <OTA>
A;Cross-references: EMBL:M82872; NID:g172293; PIDN:AAA34922.1; PID:g172294
A;Note: sequence extracted from NCBI backbone (NCBIN:88405, NCBIP:88407)
R;James, P.; Hall, B.D.; Whelen, S.; Craig, E.A.
submitted to the EMBL Data Library, July 1991
A;Description: Multiple protein tyrosine phosphatase-encoding genes in the yeast Sacchar
A;Reference number: S31554
A;Accession: S31554
A;Molecule type: DNA
A;Residues: 1-370,'S',372-659,'GA',662-750 <JAM>
A;Cross-references: EMBL:M38723; NID:g172381; PID:g172382
R;James, P.; Whelen, S.; Hall, B.D.
J. Biol. Chem. 266, 5616-5624, 1991
A;Title: The RET1 gene of yeast encodes the second-largest subunit of RNA polymerase III
A;Reference number: S14169; MUID:91170230; PMID:2005101
A;Accession: S14170
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-67 <JBI>
A;Cross-references: EMBL:M38723
R;James, P.; Hall, B.D.; Whelen, S.; Craig, E.A.
Gene 122, 101-110, 1992
A;Title: Multiple protein tyrosine phosphatase-encoding genes in the yeast Saccharomyces
A;Reference number: JC1484; MUID:93083970; PMID:1452018
A;Accession: JC1484
A;Molecule type: DNA
A;Residues: 1-370,'S',372-659,'GA',662-750 <JAW>
C;Genetics:
A;Gene: SGD:PTP2
A;Cross-references: SGD:S0005734; MIPS:YOR208w
A;Map position: 15R
C;Keywords: cell division control; nucleotide binding; phosphoprotein; phosphoric monoes
F;408-726/Domain: protein-tyrosine-phosphatase homology <PTP>
F;669-674/Region: nucleotide binding #status predicted
F;666/Active site: Cys (phosphocysteine intermediate) #status predicted
F;672/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 12; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCSAGCGRTGV 238
||||||||||||
Db 664 VHCSAGCGRTGV 675

Search completed: December 7, 2004, 09:59:57
Job time : 20 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 7, 2004, 09:50:28 ; Search time 77 Seconds
(without alignments)
3422.358 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 458
Sequence: 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 12

Total number of hits satisfying chosen parameters: 17

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	458	100.0	458	1	PTNI_HUMAN	Q99952 homo sapien
2	217	47.4	351	2	Q7Z637	Q7z637 homo sapien
3	217	47.4	372	2	Q8TA96	Q8ta96 homo sapien
4	32	7.0	453	2	Q61152	Q61152 mus musculu
5	32	7.0	453	2	Q922E3	Q922e3 mus musculu
6	29	6.3	453	2	P70602	P70602 rattus norv
7	12	2.6	258	2	Q90Y62	Q90y62 brachydanio
8	12	2.6	487	2	Q9NL13	Q9nl13 branchiosto
9	12	2.6	570	2	Q6PEI4	Q6pei4 brachydanio
10	12	2.6	570	2	AAH58051	Aah58051 brachydan
11	12	2.6	572	2	Q6NZ14	Q6nz14 brachydanio
12	12	2.6	572	2	AAH66385	Aah66385 brachydan
13	12	2.6	684	2	Q6FLK0	Q6flk0 candida gla
14	12	2.6	750	1	PTP2_YEAST	P29461 saccharomyc
15	12	2.6	799	2	Q75BW3	Q75bw3 ashbya goss
16	12	2.6	799	2	AAS51384	Aas51384 ashbya go
17	12	2.6	903	2	Q6CRT4	Q6crt4 kluyveromyc

ALIGNMENTS

RESULT 1
PTNI_HUMAN
ID PTNI_HUMAN STANDARD; PRT; 458 AA.
AC Q99952;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 18 (EC 3.1.3.48)
DE (Brain-derived phosphatase).
GN Name=PTPN18; Synonyms=BDP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=97108674; PubMed=8950995;
RA Kim Y.W., Wang H.Y., Sures I., Lammers R., Martell K.J., Ullrich A.;
RT "Characterization of the PEST family protein tyrosine phosphatase
RT BDP1.";
RL Oncogene 13:2275-2279(1996).
CC -!- FUNCTION: Differentially dephosphorylate autophosphorylated
CC tyrosine kinases which are known to be overexpressed in tumor
CC tissues.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: Expressed in brain, colon and several tumor-
CC derived cell lines.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class 4 subfamily.
CC ---

CC ---
DR EMBL; X79568; CAA56105.1; -.
DR HSSP; Q06124; 2SHP.
DR Genew; HGNC:9649; PTPN18.
DR MIM; 606587; -.
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPHTASE.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Protein phosphatase.
FT DOMAIN 26 291 Protein-tyrosine phosphatase.
FT ACT_SITE 229 229 Phosphocysteine intermediate (By
FT similarity).
SQ SEQUENCE 458 AA; 50384 MW; 46BCA1E17C2C78B1 CRC64;

Query Match 100.0%; Score 458; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60

Qy         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120

Qy        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180

Qy        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC 240

Qy        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300

Qy        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360

Qy        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420

Qy        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |||||||||||||||||||||||||||||||||||||
Db        421 SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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RESULT 2
Q7Z637
ID Q7Z637 PRELIMINARY; PRT; 351 AA.
AC Q7Z637;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PTPN18 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC052800; AAH52800.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 351 AA; 38317 MW; 5FE9B48C5D0667C4 CRC64;

Query Match 47.4%; Score 217; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 1e-207;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        139 KRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDR 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         32 KRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDR 91

Qy        199 GVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDF 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDF 151

Qy        259 SLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDAL 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 SLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDAL 211

Qy        319 FLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYA 355
              |||||||||||||||||||||||||||||||||||||
Db        212 FLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYA 248
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RESULT 3
Q8TA96
ID Q8TA96 PRELIMINARY; PRT; 372 AA.
AC Q8TA96;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to protein tyrosine phosphatase, non-receptor type 18 (Brain-
DE derived) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC024280; AAH24280.1; -.
DR EMBL; BC041562; AAH41562.1; -.
DR HSSP; P18031; 1C88.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPHTASE.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Receptor.
FT NON_TER 1 1
SQ SEQUENCE 372 AA; 40708 MW; 417CA80AA054CF8B CRC64;

Query Match 47.4%; Score 217; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.1e-207;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        139 KRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDR 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         53 KRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDR 112

Qy        199 GVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDF 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 GVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDF 172

Qy        259 SLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDAL 318
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 SLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDAL 232

Qy        319 FLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYA 355
                 |||||||||||||||||||||||||||||||||||
Db        233 FLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYA 269


RESULT 4
Q61152
ID   Q61152      PRELIMINARY;      PRT;   453 AA.
AC   Q61152; Q62404;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver
DE   phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
GN   Name=Ptpn18; Synonyms=Ptpk1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYO;
RX   MEDLINE=96329547; PubMed=8695832;
RA   Cheng J., Daimaru L., Fennie C., Lasky L.A.;
RT   "A novel protein tyrosine phosphatase expressed in
RT   lin(lo)CD34(hi)Sca(hi) hematopoietic progenitor cells.";
RL   Blood 88:1156-1167(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE=97030045; PubMed=8875997;
RA   Huang K., Sommers C.L., Grinberg A., Kozak C.A., Love P.E.;
RT   "Cloning and characterization of PTP-K1, a novel nonreceptor protein
RT   tyrosine phosphatase highly expressed in bone marrow.";
RL   Oncogene 13:1567-1573(1996).
RN   [3]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   STRAIN=C57BL/6; TISSUE=FETAL LIVER;
RX   MEDLINE=97131769; PubMed=8977243;
RA   Dosil M., Leibman N., Lemischka I.R.;
RT   "Cloning and characterization of fetal liver phosphatase 1, a nuclear
RT   protein tyrosine phosphatase isolated from hematopoietic stem cells.";
RL   Blood 88:4510-4525(1996).
CC   -!- FUNCTION: MAY BE INVOLVED IN GROWTH AND DIFFERENTIATION OF
CC       HEMATOPOIETIC CELLS.
CC   -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
CC       TYROSINE + PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=FLP1A;
CC         IsoId=Q61152-1; Sequence=Displayed;
CC       Name=FLP1B;
CC         IsoId=Q61152-2; Sequence=VSP_050405;
CC   -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BONE MARROW. ALSO
CC       EXPRESSED IN KIDNEY, LUNG, OVARY, SPLEEN, THYMUS AND LYMPH NODE.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 15.5.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY.
DR   EMBL; U35124; AAB82736.1; -.
DR   EMBL; U49853; AAB18623.1; -.
DR   EMBL; U52523; AAC52991.1; -.
DR   HSSP; Q06124; 2SHP.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Alternative splicing; Hydrolase; Nuclear protein.
FT   DOMAIN       56    290       PROTEIN-TYROSINE PHOSPHATASE.
FT   DOMAIN      312    428       PRO/SER/THR-RICH.
FT   ACT_SITE    229    229       BY SIMILARITY.
FT   VARSPLIC      9     32       Missing (in isoform FLP1B).
FT                                /FTId=VSP_050405.
FT   CONFLICT     11     11       F -> L (IN REF. 3).
FT   CONFLICT    362    368       ASAGTGP -> LRRHRA (IN REF. 3).
SQ   SEQUENCE   453 AA;  50201 MW;  88AD7E73CE8136B0 CRC64;

  Query Match             7.0%;  Score 32;  DB 2;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-22;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        100 AYIATQGPLPHTLLDFWRLVWEFGVKVILMAC 131
                 ||||||||||||||||||||||||||||||||
Db        100 AYIATQGPLPHTLLDFWRLVWEFGVKVILMAC 131


RESULT 5
Q922E3
ID   Q922E3      PRELIMINARY;      PRT;   453 AA.
AC   Q922E3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ptpn18 protein.
GN   Name=Ptpn18;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC008512; AAH08512.1; -.
DR   HSSP; Q06124; 2SHP.
DR   MGD; MGI:108410; Ptpn18.
DR   GO; GO:0005737; C:cytoplasm; IDA.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.
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DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Hydrolase.
SQ   SEQUENCE   453 AA;  50227 MW;  722FDE1FFC9F4689 CRC64;

  Query Match             7.0%;  Score 32;  DB 2;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-22;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        100 AYIATQGPLPHTLLDFWRLVWEFGVKVILMAC 131
              ||||||||||||||||||||||||||||||||
Db        100 AYIATQGPLPHTLLDFWRLVWEFGVKVILMAC 131


RESULT 6
P70602
ID   P70602      PRELIMINARY;      PRT;   453 AA.
AC   P70602;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Protein tyrosine phosphatase 20.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97067206; PubMed=8910608;
RA   Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RT   "The novel protein-tyrosine phosphatase PTP20 is a positive regulator
RT   of PC12 cell neuronal differentiation.";
RL   J. Biol. Chem. 271:29422-29426(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Aoki, N, Yamaguchi-Aoki, Y, Ullrich A.;
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U69673; AAC52896.1; -.
DR   HSSP; Q06124; 2SHP.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR   GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Hydrolase.
SQ   SEQUENCE   453 AA;  50106 MW;  6CCC132206FB69AE CRC64;

  Query Match             6.3%;  Score 29;  DB 2;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-19;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        430 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
              |||||||||||||||||||||||||||||
Db        425 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453


RESULT 7
Q90Y62
ID   Q90Y62      PRELIMINARY;      PRT;   258 AA.
AC   Q90Y62;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Receptor PTP-like protein IA-2 (Fragment).
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21076097; PubMed=11206415;
RA   Cai T., Krause M.W., Odenwald W.F., Toyama R., Notkins A.L.;
RT   "The IA-2 gene family: homologs in Caenorhabditis elegans, Drosophila
RT   and zebrafish.";
RL   Diabetologia 44:81-88(2001).
DR   EMBL; AF190144; AAL05974.1; -.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Hydrolase; Receptor.
FT   NON_TER       1       1.
SQ   SEQUENCE   258 AA;  29544 MW;  93FBC53CAA4EA4A2 CRC64;

  Query Match             2.6%;  Score 12;  DB 2;  Length 258;
  Best Local Similarity   100.0%;  Pred. No. 0.0068;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        100 AYIATQGPLPHT 111
              ||||||||||||
Db         58 AYIATQGPLPHT 69


RESULT 8
Q9NL13
ID   Q9NL13      PRELIMINARY;      PRT;   487 AA.
AC   Q9NL13;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   AmPTPR4c protein (Fragment).
GN   Name=amPTPR4c;
OS   Branchiostoma belcheri (Amphoxius).
OC   Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC   Branchiostoma.
OX   NCBI_TaxID=7741;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20219325; PubMed=10754074;
RA   Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT   "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT   divergence of tissue-specific isoform genes in the early evolution of
RT   vertebrates.";
RL   J. Mol. Evol. 50:302-311(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ono K.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB033564; BAA95171.1; -.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR   GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 2.
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DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 2.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW   Hydrolase.
FT   NON_TER       1      1
SQ   SEQUENCE   487 AA;  55573 MW;  CF2BCC6D933C6ADD CRC64;

  Query Match             2.6%;  Score 12;  DB 2;  Length 487;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        100 AYIATQGPLPHT 111
              ||||||||||||
Db        267 AYIATQGPLPHT 278


RESULT 9
Q6PEI4
ID   Q6PEI4      PRELIMINARY;      PRT;   570 AA.
AC   Q6PEI4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Protein tyrosine phosphatase, non-receptor type 12.
GN   Name=ptpn12;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC058051; AAH58051.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003595; PTPc_motif.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   SMART; SM00404; PTPc_motif; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Hydrolase; Receptor.
SQ   SEQUENCE   570 AA;  64502 MW;  19D2959EEFC5F02B CRC64;

  Query Match             2.6%;  Score 12;  DB 2;  Length 570;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        226 CVHCSAGCGRTG 237
              ||||||||||||
Db        225 CVHCSAGCGRTG 236


RESULT 10
AAH58051
ID   AAH58051    PRELIMINARY;      PRT;   570 AA.
AC   AAH58051;
DT   24-MAY-2004 (TrEMBLrel. 27, Created)
DT   24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT   24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE   Protein tyrosine phosphatase, non-receptor type 12.
GN   PTPN12.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC058051; AAH58051.1; -.
KW   Receptor.
SQ   SEQUENCE   570 AA;  64502 MW;  19D2959EEFC5F02B CRC64;

  Query Match             2.6%;  Score 12;  DB 2;  Length 570;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        226 CVHCSAGCGRTG 237
              ||||||||||||
Db        225 CVHCSAGCGRTG 236


RESULT 11
Q6NZ14
ID   Q6NZ14      PRELIMINARY;      PRT;   572 AA.
AC   Q6NZ14;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
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DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ptpn12 protein.
GN   Name=ptpn12;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Strausberg R.;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC066385; AAH66385.1; -.
DR   InterPro; IPR003595; PTPc_motif.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   SMART; SM00404; PTPc_motif; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Hydrolase.
SQ   SEQUENCE   572 AA;  64712 MW;  365E6E9B742316B7 CRC64;

  Query Match             2.6%;  Score 12;  DB 2;  Length 572;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        226 CVHCSAGCGRTG 237
              ||||||||||||
Db        225 CVHCSAGCGRTG 236


RESULT 12
AAH66385
ID   AAH66385    PRELIMINARY;      PRT;   572 AA.
AC   AAH66385;
DT   24-MAY-2004 (TrEMBLrel. 27, Created)
DT   24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT   24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ptpn12 protein.
GN   PTPN12.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Strausberg R.;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC066385; AAH66385.1; -.
SQ   SEQUENCE   572 AA;  64712 MW;  365E6E9B742316B7 CRC64;

  Query Match             2.6%;  Score 12;  DB 2;  Length 572;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        226 CVHCSAGCGRTG 237
              ||||||||||||
Db        225 CVHCSAGCGRTG 236


RESULT 13
Q6FLK0
ID   Q6FLK0      PRELIMINARY;      PRT;   684 AA.
AC   Q6FLK0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Strain CBS138 chromosome L complete sequence.
GN   ORFNames=CAGL0L02827g;
OS   Candida glabrata (Yeast) (Torulopsis glabrata).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=5478;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CBS138;
RG   GENOLEVURES;
RA   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA   Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA   Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA   Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA   Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA   Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA   Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA   Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA   Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA   Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA   Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA   Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA   Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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RA   Wincker P., Souciet J.L.;
RT   "Genome evolution in yeasts.";
RL   Nature 430:35-44(2004).
DR   EMBL; CR380958; CAG61864.1; -.
DR   InterPro; IPR003595; PTPc_motif.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   SMART; SM00404; PTPc_motif; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Hydrolase.
SQ   SEQUENCE   684 AA;  78640 MW;  CAFBE6EC6BD2D23E CRC64;

  Query Match             2.6%;  Score 12;  DB 2;  Length 684;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VHCSAGCGRTGV 238
              ||||||||||||
Db        596 VHCSAGCGRTGV 607


RESULT 14
PTP2_YEAST
ID   PTP2_YEAST     STANDARD;      PRT;   750 AA.
AC   P29461;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Protein-tyrosine phosphatase 2 (EC 3.1.3.48) (PTPase 2).
GN   Name=PTP2; OrderedLocusNames=YOR208W;
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92250559; PubMed=1577774;
RA   Guan K., Deschenes R.J., Dixon J.E.;
RT   "Isolation and characterization of a second protein tyrosine
RT   phosphatase gene, PTP2, from Saccharomyces cerevisiae.";
RL   J. Biol. Chem. 267:10024-10030(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92196117; PubMed=1549598;
RA   Ota I.M., Varshavsky A.;
RT   "A gene encoding a putative tyrosine phosphatase suppresses lethality
RT   of an N-end rule-dependent mutant.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:2355-2359(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   James P., Hall B.D., Whelen S., Craig E.A.;
RL   Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Hughes B., Pohl T.M.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May be implicated in the ubiquitin-mediated protein
CC       degradation pathway. May be involved in the regulation of MAP
CC       kinase FUS3.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC       Non-receptor class subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M85287; -; NOT_ANNOTATED_CDS.
DR   EMBL; M82872; AAA34922.1; -.
DR   EMBL; M38723; AAB59323.1; -.
DR   EMBL; Z75116; CAA99423.1; -.
DR   PIR; S67100; S67100.
DR   HSSP; P18052; 1YFO.
DR   GermOnline; 143796; -.
DR   SGD; S0005734; PTP2.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Hydrolase; Protein phosphatase.
FT   ACT_SITE    666    666       Phosphocysteine intermediate (By
FT                                similarity).
FT   CONFLICT    371    371       L -> S (in Ref. 3).
FT   CONFLICT    474    475       KL -> NV (in Ref. 1).
FT   CONFLICT    660    661       SP -> GA (in Ref. 3).
SQ   SEQUENCE   750 AA;  85868 MW;  1033D2F0AA23BD35 CRC64;

  Query Match             2.6%;  Score 12;  DB 1;  Length 750;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VHCSAGCGRTGV 238
              ||||||||||||
Db        664 VHCSAGCGRTGV 675


RESULT 15
Q75BW3
ID   Q75BW3       PRELIMINARY;      PRT;   799 AA.
AC   Q75BW3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ACR158Wp.
GN   Name=ACR158W;
OS   Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX   NCBI_TaxID=33169;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 10895;
RX   PubMed=15001715;
RA   Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA   Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
RA   Gaffney T.D., Philippsen P.;
RT   "The Ashbya gossypii genome as a tool for mapping the ancient
RT   Saccharomyces cerevisiae genome.";
RL   Science 304:304-307(2004).
DR   EMBL; AE016888; AAS51384.1; -.
DR   AGD; ACR158W; -.
DR   InterPro; IPR003595; PTPc_motif.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00194; PTPc; 1.
DR   SMART; SM00404; PTPc_motif; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
```

```
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW   Hydrolase.
SQ   SEQUENCE   799 AA;  89345 MW;  A619E56C3C969640 CRC64;

  Query Match           2.6%;  Score 12;  DB 2;  Length 799;
  Best Local Similarity  100.0%;  Pred. No. 0.018;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VHCSAGCGRTGV 238
              ||||||||||||
Db        713 VHCSAGCGRTGV 724


RESULT 16
AAS51384
ID   AAS51384    PRELIMINARY;      PRT;   799 AA.
AC   AAS51384;
DT   23-APR-2004 (TrEMBLrel. 27, Created)
DT   23-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   23-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   ACR158Wp.
GN   ACR158W.
OS   Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX   NCBI_TaxID=33169;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 10895;
RX   PubMed=15001715;
RA   Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA   Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
RA   Gaffney T.D., Philippsen P.;
RT   "The Ashbya gossypii genome as a tool for mapping the ancient
RT   Saccharomyces cerevisiae genome.";
RL   Science 304:304-307(2004).
DR   EMBL; AE016888; AAS51384.1; -.
SQ   SEQUENCE   799 AA;  89345 MW;  A619E56C3C969640 CRC64;

  Query Match           2.6%;  Score 12;  DB 2;  Length 799;
  Best Local Similarity  100.0%;  Pred. No. 0.018;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VHCSAGCGRTGV 238
              ||||||||||||
Db        713 VHCSAGCGRTGV 724


RESULT 17
Q6CRT4
ID   Q6CRT4      PRELIMINARY;      PRT;   903 AA.
AC   Q6CRT4;
DT   01-OCT-2004 (TrEMBLrel. 28, Created)
DT   01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Strain NRRL Y-1140 chromosome D of strain NRRL Y-1140 of Kluyveromyces
DE   lactis.
GN   ORFNames=KLLA0D06611g;
OS   Kluyveromyces lactis (Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX   NCBI_TaxID=28985;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRRL Y-1140;
RG   GENOLEVURES;
RA   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA   Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA   Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA   Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA   Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA   Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA   Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA   Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA   Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA   Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA   Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA   Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA   Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA   Wincker P., Souciet J.L.;
RT   "Genome evolution in yeasts.";
RL   Nature 430:35-44(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRRL Y-1140;
RA   Genoscope;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR382124; CAH00451.1; -.
SQ   SEQUENCE   903 AA;  102110 MW;  5E71496FAE5D6197 CRC64;

  Query Match           2.6%;  Score 12;  DB 2;  Length 903;
  Best Local Similarity  100.0%;  Pred. No. 0.02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VHCSAGCGRTGV 238
              ||||||||||||
Db        823 VHCSAGCGRTGV 834


Search completed: December  7, 2004, 09:59:33
Job time : 78 secs
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